Nashed Seg 102,142

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

February 8, 2003, 04:17:29; Search time 3114 Seconds (without alignments) 4093.526 Million cell updates/sec Run on:

US-09-975-456B-1 507

1 atgaagaagttcttcaccgt......cgccccccgccctcctag 507 Perfect score:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

24791104 seqs, 12571243825 residues Searched:

49582208 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database :

/cgn2_6/ptcdata/2/pna/US100A_COMB.seq:*
/cgn2_6/ptcdata/2/pna/US100B_COMB.seq:*
/cgn2_6/ptcdata/2/pna/US100B_COMB.seq:*
/cgn2_6/ptcdata/2/pna/US101B_COMB.seq:*
/cgn2_6/ptcdata/2/pna/US101B_COMB.seq:*
/cgn2_6/ptcdata/2/pna/US102A_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Match Length DB ID Match Length DB ID Match Length DB ID 100.0 2270 64 US-09-975-456B-1 100.0 2270 64 US-0-203-511-4 100.0 2270 64 US-0-10-10-10-10-10-10-10-10-10-10-10-10-1								_	_		_	_	_	_	_						_	_	_
Score Match Length DB ID Score Match III-4 Score III-6 Score Match III-4 Score III-6 Score III-		;	pp11	pp1.1	ppl1	, Ap	App	App	App	7, A	App			-	-					Appl	App	App	7, A
Score Match Length DB ID 507 100.0 2270 64 US-60-203-511-4 507 100.0 2270 64 US-60-203-511-4 507 100.0 2270 64 US-60-203-511-4 507 100.0 2270 84 US-60-203-511-4 505.4 99.7 2716 40 US-10.104 0.47-71765 464 91.5 748 65 US-60-212-356-317 464 91.5 829 65 US-60-212-356-317 342.2 67.5 903 80 US-60-229-525-724 252.4 49.8 748 66 US-60-229-525-724 252.4 49.8 748 66 US-60-234-446-1225 240 47.3 256 67 US-60-234-446-1225 212 41.8 4179 64 US-60-136-590-447 199.4 39.3 1644 23 US-96-609-137-56 1167.2 33.0 :388 23 US-99-609-137-38 125 24.9 549 63 US-60-196-174-103		:	1, A	4, A	3, A	1765	317,							447,	829,	43,	26,	56,	38,	38,	103,	686,	1564
Score Match Length DB ID 507 100.0 2270 64 US-60-203-511-4 507 100.0 2270 64 US-60-203-511-4 507 100.0 2270 64 US-60-203-511-4 507 100.0 2270 84 US-60-203-511-4 505.4 99.7 2716 40 US-10.104 0.47-71765 464 91.5 748 65 US-60-212-356-317 464 91.5 829 65 US-60-212-356-317 342.2 67.5 903 80 US-60-229-525-724 252.4 49.8 748 66 US-60-229-525-724 252.4 49.8 748 66 US-60-234-446-1225 240 47.3 256 67 US-60-234-446-1225 212 41.8 4179 64 US-60-136-590-447 199.4 39.3 1644 23 US-96-609-137-56 1167.2 33.0 :388 23 US-99-609-137-38 125 24.9 549 63 US-60-196-174-103		lpt lon	nence	rence	nence	nence	nence	nence	nence	nence	Jence	nence	nence	nence	nence	nence	nence	uence	uence	uence	nence	uence	Sequence
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No.		Score	507	507	507	505.4	464	464	379	342.2	305	252.4	240	222.8	212	212	199.4	199.4	167.2	167.2	126	115	110.8
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421 CCCACGCCCAACTGCAGCATCTATGAACCGCCCCTGAGGAGGTCACCTGCAGTCACGAA 480

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Sequence 4, Application US/60203511 GENERAL INFORMATION:

US-60-203-511-4

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Sequence 15647, A Sequence 22948, A Sequence 22948, A Sequence 22948, A Sequence 22948, A Sequence 31852, A Sequence 70519, A Sequence 70519, A Sequence 30282, A Sequence 30282, A Sequence 68551, A Sequence 67, Appli Sequence 67, Appli Sequence 67, Appli Sequence 281, Appli Sequence 57, Appli Sequence 91, Appli Sequence	
560 38 US-10-027-632-15647 549 17 US-09-362-510-22948 549 18 US-09-362-510-22948 549 34 US-09-362-510-22948 549 35 US-09-948-413-2948 674 19 US-09-904-413-22948 674 35 US-09-943-413-8143 674 35 US-09-943-524-31852 451 19 US-09-933-524-31852 451 35 US-09-933-524-70519 476 18 US-09-933-524-70519 476 35 US-09-933-524-68551 719 35 US-09-933-524-68551 719 35 US-09-933-524-68551 854 36 US-09-933-524-68551 854 36 US-09-933-524-68551 854 36 US-09-933-524-68551 854 36 US-09-933-524-68551 857 US-09-933-524-68551 858 35 US-09-933-524-68551 858 35 US-09-933-524-68551 859 US-09-933-524-68551 851 US-09-933-524-68551 852 US-09-933-524-68551 853 US-09-933-524-68551 854 36 US-09-933-524-68551 857 US-09-933-524-68551 858 35 US-09-935-524-68551 858 35 US-09-935-524-68551 858 35 US-09-935-524-68551 859 US-09-935-524-68551	
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1000 1000 1000 99 99 99 99 99 99 99 99 99 99 99 99	
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ALIGNMENTS

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APPLICANT: LAZDUNSKI, MICHEL
APPLICANT: LAMBEAU, GERARD
APPLICANT: LAMBEAU, GERARD
APPLICANT: LAMBEAU, GERARD
TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
FILE REPERENCE: 1478-R-0
CURRENT APPLICATION NUMBER: US/09/975,456B
PRIOR APPLICATION NUMBER: 60/239,491
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PAGENTIN VERSION 2.1
SOFTWARE: PAGENTIN VERSION 2.1
                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1)..(507); OTHER INFORMATION: CDNA encoding human group IIF secreted phospholipase A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGAGCGCCATCCTGTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGAAGAAGITCITCACCGIGGCCATCCTTGCTGGCAGGGTTCTGTCCACAGCTCACGGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 507; DB 36; Length 507; 100.0%; Pred. No. 1.1e-115; tive 0; Mismatches 0; Indels 0;
                            ; Sequence 1, Application US/09975456B; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 507; Conservative
                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
RESULT 1
US-09-975-456B-1
                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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61 ACCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGAGCGCCCATCCTGTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                     121 TTCGTGGGCTACGGTTGCTACTGTGGGGCGGGCGGTGGCCAGCCCAAGGATGAGGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                  181 GACTGGTGCCGCCACGACTGCTGCTACCAGGAACTCTTTGACCAAGGCTGTCAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                               402 GACTGGTGCTGCCACGCCCCACGACTGCTGCTACCAGGAACTCTTTGACCAAGGCTGTGTACA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 CCCIATGTGGACCACTATGATCACACCATCGAGAACAACACTGAGATAGTCTGCAGTGAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2270;
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                                                                                                                                                                                                                                                             Ouery Match 100.0%; Score 507; DB 64; Best Local Similarity 100.0%; Pred. No. 1.5e-115; Matches 507; Conservative 0; Mismatches 0;
                                                                APPLICANT: Yue, Henry
APPLICANT: Khan, Farrah A.
TITLE OF INVENTION: LIPID METABOLISM ENZYMES
FILE REFERENCE: PI-0095 p
                                                                                                                                                                                                                 NAME/KEY:
OTHER INFORMATION: Incyte ID No: 7473224CB1
                                                                                                FILE REFERENCE: PI-0095 P
CURRENT APPLICATION NUMBER: US/60/203,511
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
                                                   Lu, Yan
Tribouley, Catherine M.
APPLICANT: Das, Debopriya
APPLICANT: Reddy, Roopa
APPLICANT: Yao, Monique G.
                                                                                                                                                                                 TYPE: DNA
ORGANISM: HOMO sapiens
                                                                                                                                         NUMBERS PERL SOFTWARE: PERL SEQ ID NO 4
                                             APPLICANT:
APPLICANT:
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301 CTCAACAAGACAGAGTGTGACAAGCAGACATGTGTGTGACAAGAACATGGTTCTGTGC 360
                                                         361 CTCATGAACCAGACGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCCAGGGC 420
                                                                                                                 421 CCCACGCCCAACTGCAGCATCTATGAACCGCCCCTGAGGAGGTCACCTGCAGTCACCAA 480
                  61 AGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGAGGAGGGCGCCATCCTGTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGAAGAAGTICTICACCGIGGCCAICCTIGCTGGCAGCGTICTGICCACAGCICACGGC 60
                                                                                                                                                                                                                                                                            Sequence 3, Application US/60403468
GENERAL INFORMATION:
APPLICANT: S1los-Santiago, Inmaculada
TITLE OF INVENTION: Methods and compositions for treating
TITLE OF INVENTION: u.o.logical disorders using 260, 55089 or 21407
FILE REPRENCE: MP102-148P1(M)
CURRENT APPLICATION NUMBER: US/60/403,468
CURRENT FILING DATE: 2002-08-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 100.0%; Score 507; DB 84; Best Local Similarity 100.0%; Pred. No. 1.5e-115; Matches 507; Conservative 0; Mismatches 0;
                                                                                                                                                                          481 TCCCCAGCGCCCCCGCCCTCCCTAG 507
                                                                                                                                                                                             702 TCCCCAGCGCCCCCCCCCTCTAG 728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE TITLE OF INVENTION: PROTEINS, AND USES THEREOF FILE REFERENCE: CLOOM677 CURRENT APPLICATION NUMBER: US/60/212,356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGGCCCTGGCCAGGCAAGGATGAGGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 CCCTATGTGGACCACTATGATCACACCATCGAGAACAACACTGAGATAGTCTGCAGTGAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 CTCATGAACCAGACGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCCAGGGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 CCCACGCCCAACTGCAGCATCTATGAACCGCCCCTGAGGAGGTCACCTGCAGTCACCAA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.7%; Score 505.4; DB 40; Length 2716; 99.8%; Pred. No. 3.8e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                        APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REPERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  712 TCCCCAGCGCCCCCCCCCTCCTAG 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 TCCCCAGCGCCCCCCCCTCCTAG 507
                       Sequence 1765, Application US/10104047 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 317, Application US/60212356
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.89
Matches 506; Conservative
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                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
US-10-104-047-1765
                                                                                                                                                                                                                                                                                                                              US-10-104-047-1765
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                                                                                                                                                                                                                                                                    2716
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TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLOOG677
CURRENT APPLICATION NUMBER: US/60/212,356
NUMBER OF SEQ ID NOS: 411
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                 61 AGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGAGGGCGCCATCCTGTCC 120
                                                                                                                                                                                                                                                                                        121 TICCIGGGCTACGGTIGCTACTGTGGGGCTGGGGGCCGTGGCCAGGCCCAAGGATGAGGTG 180
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                             181 GACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAACTCTTTGACCAAGGCTGTCAC 240
                                                                                                                                                                                                                                                                                                                                                              241 CCCTATGTGGACCACTATGATCACACCATCGAGAACAACAACAGGAGATAGTCTGCAGTGAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGAAGAAGTICTICACCGTGGCCATCCTTGCTGGCAGCGTTCTGTCCACAGCTCACGGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 CTCAACAAGACAGAGTGTGACAAGCAGACATGCATGTGTGACAAGAACATGGTTCTGTGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 CTCATGAACCAGACGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCCAGGGC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AIGAAGAAGTICTICACCGIGGCCAICCTIGCIGGCAGCGIICTGICCACAGCTCACGGC 60
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                                                                                                                                     Length 748;
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100.0%; Pred. No. 5.9e-105;
Live 0; Mismatches 0; Indels
                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 CCCACGCCCAACTGCAGCATCTATGAACCGCCCCTGAGGAGGT 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.5%; Score 464; DB 65; L
100.0%; Pred. No. 5.8e-105;
Live 0; Mismatches 0;
             NUMBER OF SEQ ID NOS: 411
SOFTWARE: FastSEQ for Windows Version 4.0
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; GENERAL INFORMATION:
    2000-06-19
                                                                                                                                                          Conservative
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CURRENT FILING DATE:
                                                                                                                                        Similarity
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                                                                                  ; ORGANISM: HUMAN
US-60-212-356-317
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US-60-212-356-282
                                        SEQ ID NO 317
LENGTH: 748
                                                                                                                                                     464;
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                                                                     TYPE: DNA
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Best Local (
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Sequence 741, Application US/60229525
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/229,525
CURRENT APPLICATION NUMBER: US/60/229,525
NUMBER OF SEQ ID NOS: 819
SOFTWARE: FastSEQ for Windows Version 4.0
AGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGAGGAGCGCCATCCTGTCC 120
              121 TTCGTGGGCTACGGTTGCTACTGTGGGGCTGGGGGCCGTGGCCAGCCCAAGGATGAGGTG 180
                                                                    181 GACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAACTCTTTGACCAAGGCTGTCAC 240
                                                                                                                         241 CCCTATGTGGACCACTATGATCACACCATCGAGAACAACACGGGAGATAGTCTGCAGTGAC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.8%; Score 379; DB 66; Length 379; 100.0%; Pred. No. 7.1e-84; ative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                          421 CCCACGCCCAACTGCAGCATCTATGAACCGCCCCTGAGGAGGT 464
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LENGTH: 379
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ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
PROTEINS, AND USES THEREOF
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                                                                                                                                                   Sequence 10397, Application US/60360207
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
FILE REFERENCE: CL001321
CURRENT APPLICATION NUMBER: US/60/360,207
CURRENT APPLICATION UNDER: 2002-03-01
NUMBER OF SEQ ID NOS: 47235
SEQ ID NO 10397
                                                                                                                                                                                                                                                                                                                                                                            67.5%; Score 342.2; DB 80; Length 903; 79.7%; Pred. No. 1.2e-74; tive 0; Mismatches 103; Indels 0;
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                                                              361 GGGCCCCACGCCCAACTGC 379
                                              417 GGCCCCACGCCCAACTGC 435
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Matches 404; Conservative
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TITLE OF INVENTION: ISOLAT
TITLE OF INVENTION: NUCLEI
TITLE OF INVENTION: PROTEI
                                                                                                                        RESULT 8
US-60-360-207-10397
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US-60-360-207-10397
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TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000772
                                                                                                                                                                                                                                                                                                                                                              91 GCCGTCACAGGGAGGAGCGCCATCCTGTCGTGGGCTACGGTTGCTACTGTGGGCTG 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 GAGAACAACACTGAGATAGTCTGCAGTGAGTCCCTCCCCTGTCACCTGGGCCCCCAGAGA 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                              60.2%; Score 305; DB 66; Length 748; 83.2%; Pred. No. 2.1e-65; Live 0; Mismatches 70; Indels
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FILE REFERENCE: CL000772
CURRENT APPLICATION NUMBER: US/60/229,525
CURRENT APPLICATION DATE: 2000-09-05
NUMBER OF SEO ID NOS: 819
SOFTWARE: FastSEO for Windows Version 4.0
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CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 819
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                                                                                                                                                                                                                                  Matches 347; Conservative
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Matches 304; Conservative
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                                                                                                                                           ORGANISM: HUMAN
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                                                                                                                                                            US-60-229-525-724
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US-60-229-525-571
                                                                                                      LENGTH: 748
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                                                                                       SEQ ID NO 724
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LENGTH: 748
                                                                                                                           TYPE: DNA
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Dufour, Gerard E.
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Best Local Similarity
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TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO00832
CURRENT PAPLICATION NUMBER: US/60/234,446
CURRENT FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 1797
SSETWARE: FastSEQ for Windows Version 4.0
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0
160 GGCCAGCCCAAGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAA 219
                                              220 CICITIGACCAAGGCIGICACCCCIAIGIGGACCACIAIGAICACACCAICGAGAACAAC 279
                                                                                               340 GACAAGAACATGGTTCTGTGCCTCATGAACCAGACGTACCGAGAGAAGTACCGTGGCTTC 399
                                                                                                                                                                                                           60 CAGCCIGCICAACCIGAAGGCCAIGGIGGAGGCCGICACAGGGAGGAGGAGCGCCAICCIGIC 119
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                                                                                                                                                                                                                                                 400 CTCAATGTCTACTGCCAGGGCCCCACGCCC 429
                                                                                                                                                                                                                                                                           580 CTCAATGTCTACTAATAAAGGCCTCCTACC 609
                                                                                                                                                                                                                                                                                                                                              Sequence 1225, Application US/60234446 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 240; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: HUMAN
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APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000116
CURRENT APPLICATION NUMBER: US/60/160,203
CURRENT PILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 6374
SEQ ID NOS: 6374
SEQ ID NO 829
LENGTH: 627
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ITCGTGGGCTACGGTTGCTACTGTGGGCGGGGCCGTGGCCAG-CCCAAGGATGAGGT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 GGACTGGTGCTGCCACGCCCACGACTGCTACCAGGAACTCTTTGACCAA--GGCTGT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGAAGAAGTTCTTCACCGTGGCCATCCTTGCTGGCAGCGTTCTGTCCACAGGTCACGGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.9%; Score 222.8; DB 56; Length 483; 95.4%; Pred. No. 5.6e-45; Live 0; Mismatches 9; Indels 3;
                                                                                                                                                                         APPLICANT: Roseberry, Ana M. APPLICANT: Roseberry, Ana M. APPLICANT: Wight, Rachel J. TITLE OF INTENTION: INTRACELLULAR SIGNALLING MOLECULES FILE REFERENCE: PT-0006 P. CURRENT APPLICATION NUMBER: US/60/126,590 CURRENT FILING DATE: 1999-03-26 NUMBER OF SED ID NOS: 857 SOFTWARE: PERL Program
SEQ ID NO 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 307, 450
OTHER INFORMATION: a or g or c or t, unknown, or other
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APPLICANT: Cohen, Howard J.
APPLICANT: Rosen, Bruce
APPLICANT: Shah, Purvi
APPLICANT: Chalup, Michael S.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Jones, Anissa L.
APPLICANT: Greenawalt, Lila B.
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US-60-126-590-447
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ORGANISM: Homo sapiens
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US-60-160-203-829
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GENERAL INFORMATION:
APPLICANT: Beasley, Billen
TITLE OF INVEWTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVEWTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
TITLE OF INVEWTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO00605: US/60/207,316
CURRENT APPLICATION NUMBER: US/60/207,316
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 132
SOCTWARE: FeatSEQ for Windows Version 4.0
LENGTH: 4179
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GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-158
CURRENT APPLICATION NUMBER: US/09/609,137
CURRENT FILING DATE: 2000-06-30
NUMBER OF SEQ IN DOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
                                    0; Indels
Query Match
41.8%; Score 212; DB 60;
Best Local Similarity 100.0%; Pred. No. 2.9e-42;
Matches 212; Conservative 0; Mismatches 0;
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ORGANISM: HUMAN
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                                                                                                                                                                           105 GGTTCTGTGCCTCATGAACCAGAGGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTA 164
                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                 DB 23; Length 1644;
                                                                                            39.3%; Score 199.4; DB 2
94.9%; Pred. No. 4.8e-39;
tive 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                     471 CAGTCACCAATCCCCAGGGCCCCCCGCCCTCCCTAG 507
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                                                                                                                            Matches 206; Conservative
                                             ; ORGANISM: Homo sapiens
US-09-609-137-56
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Best Local Similarity
SEQ ID NO 56
LENGTH: 1644
                                 TYPE: DNA
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Query Match
100.0%; Score 507; DB 6; Length 2270;
Best Local Similarity 100.0%; Pred. No. 7.3e-123;
Matches 507; Conservative 0; Mismatches 0; Indels 0
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CTHER INFORMATION: Incyte ID No: 7473224CB1
US-10-275-998-7
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                  February 8, 2003, 04:36:59 ; Search time 182 Seconds (without alignments) 3602.321 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                          1 atgaagaagttcttcaccgt.......cgccccccgccctccctag 507
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1: /cgn2_6/ptodata/2/pna/VBC_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/VBC_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/VBSO_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/VBSO_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/VBSO_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/VBSO_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/VBSO_NEW_COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-188-832-79
US-10-276-781-616
US-09-949-002-228
PCT-USO2-29560-195
US-10-131-813A-533
US-10-131-813A-533
US-10-131-828A-533
US-10-131-828A-533
US-10-131-828A-533
US-10-131-828A-533
US-10-131-828A-533
US-10-125-926A-533
US-10-127-838A-533
US-10-127-838A-533
US-10-127-838A-533
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US-10-127-842A-533
US-10-127-850A-533
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                                                                                                                              OM nucleic - nucleic search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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APPLICANT: Mack, David H.

APPLICANT: Mack, David H.

APPLICANT: Aziz, Natasha

APPLICANT: Eos Biorechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

CURRENT FILING DATE: 2002-12-04

PRIOR RPLICATION NUMBER: PCT/US02/21338

CURRENT FILING DATE: 2001-07-03

PRIOR PELING DATE: 2001-07-03

PRIOR PELING DATE: 2001-07-03

PRIOR APPLICATION NUMBER: US 60/310,099

PRIOR FILING DATE: 2001-11-08

PRIOR FILING DATE: 2001-11-13

PRIOR FILING DATE: 2001-11-13

PRIOR PELING DATE: 2001-11-13

PRIOR PELING DATE: 2001-11-13

PRIOR PELING DATE: 2001-11-13

PRIOR FILING DATE: 2002-04-12
                    282 AGCCIGCICAACCIGAAGGCCAIGGIGGAGGCCGICACAGGGAGGAGGACGCCAICCTGIC 341
                                                                                                                                                                   121 TTCGTGGGCTACGGTTGCTACTGTGGGCCTGGGGGCCCGTGGCCAGCCCAAGGATGAGGTG 180
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APPLICANT: Mack, David H.
APPLICANT: Aziz, Natasha
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
TITLE OF INVENTION: Cancer
121 TTCGTGGGCTACGGTTGCTACTGTGGGCGTGGGGGCCCGTGGCCAGGCTAGGATGAGGTG 180
                                                                               241 CCCIAIGIGGACCACIAIGAICACACCATCGAGAACAACACIGAGAIAGICTGCAGIGAC 300
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CURRENT APPLICATION NUMBER: US/10/188,832
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US 60/302,814
PRIOR PELING DATE: 2001-07-03
PRIOR PELING DATE: 2001-07-03
PRIOR PELING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR PELING DATE: 2001-10-08
PRIOR APPLICATION NUMBER: US 60/343,705
PRIOR PELING DATE: 2001-11-08
PRIOR PELING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR PELING DATE: 2001-11-13
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Best Local Similarity 100.0
Matches 507; Conservative
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                          61 AGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGAGGCGCCATCCTGTCC 120
249 ATGAAGAAGTTCTTCACCGTGGCCATCCTTGCTGGCAGCGTTCTGTCCACAGCTCACGGC 308
                                      121 TTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGCCCGTGGCCAGGCCAAGGATGAGGTG 180
                                                                                         181 GACTGGTGCCACGCCCACGACTGCTGCTACCAGGAACTCTTTGACCAAGGCTGTCAC 240
                                                                                                                                           241 CCCTATGTGGACCACTATGATCACCATCGAGAACAACACTGAGATAGTCTGCAGTGAC 300
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APPLICANT: Hyseq, inc.
APPLICANT: Tang et al.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REPERENCE: 21272-018 (785 contig)
CURRENT APPLICATION NUMBER: US/10/276,781
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 2018
SOFTWARE: FastSEQ for Windows Version 3.0
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Matches 202; Conservative
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US-10-276-781-616
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOO0790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
FILE REPERENT ETLING DATE: 2000-01-28
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
FILE REFERENCE: CLOO0790
CURRENT APPLICATION UNMER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
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340 GACAAGAACATGGTTCTGTGCCTCATGAACCAGACGTACCGAGAGGAGTACCG 392
                              340 GACAAGAACATGGTTCTGTGCCTCATGAACCAGACGTACCGAGAGGAGTACCG 392
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                     Sequence 110, Application US/09949002
GENERAL INFORMATION:
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US-10-245-882-195
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APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Milson, Keith E.
APPLICANT: Zlotnik, Albert
APPLICANT: Zlotnik, Albert
APPLICANT: Destroy, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Diagnosis of Cancer, CURRENT PILING DATE: 2015-11-01
FILE REPERENCE: 018501-002710pC
CURRENT FILING DATE: 2005-11-01
FRIOR APPLICATION NUMBER: US 60/323,469
FRIOR APPLICATION NUMBER: US 60/323,469
FRIOR PILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 412
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                                                                                                                                                                                                                 6; Gaps
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                                                                                                                                                                          Length 1938;
                                                                                                                                                                        Score 99; DB 5; Length 1938
Pred. No. 2.7e-16;
0; Mismatches 145; Indels
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSEQ for Windows Version 4.0
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57.2%;
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Gish, Kurt C.
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ORGANISM: Homo sapiens
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                                                                                                                                                                                               Similarity
                                                                                                                 ; ORGANISM: Human
US-09-949-002-228
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LENGTH: 1938
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                                                                                                TYPE: DNA
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APPLICANT: Mack, David H.

APPLICANT: Mack, David H.

APPLICANT: 2lotnik, Albert

APPLICANT: Connection of Since Connection of C
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100 GGGAGGAGCGCCATCCTGTCCTTCGTGGGCTACGGTTGCTACTGTGGGCCTGGGGGGGCCGT 159
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SOFTWARE: FastSEQ for Windows Version 3.0
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Mack, David H.
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les 202; Conservative
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Gish, Kurt C.
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NAME/KEY: unsure

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160 GGCCAGCCCAAGGATGAGGTGGACTGGTGCTGCCACGCCACGACTGCTGCTACCAGGAA 219
                                                                                                                    220 CTCTTTGACCAAGGCTGTCACCCCTATGTGGACCACTATGATCACACCATGGAGAACAAC 279
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APPLICANT: Watanabe Colin K
APPLICANT: Watanabe Colin K
APPLICANT: Watanabe Colin K
APPLICANT: Wood Walliam
APPLICANT: And Good Walliam
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C139
CURRENT APPLICATION NUMBER: US/10/131,813A
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PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR PLING DATE: 1997-06-18

PRIOR PLING DATE: 1997-06-18

PRIOR PLING DATE: 1997-08-16

PRIOR APPLICATION NUMBER: 60/059113

PRIOR APPLICATION NUMBER: 60/059115

PRIOR PLING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR PLING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR PLING DATE: 1997-09-17

PRIOR PRILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-19

PRIOR FILING DATE: 1997-09-19
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APPLICANT: Beresini, Maureen
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Gurney, Austin L.
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Filvaroff, Ellen
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ORGANISM: Homo Sapien
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C134
CURRENT APPLICATION NUMBER: US/10/131,819A
CURRENT FILING DATE: 2002-04-24
PRICR APPLICATION NUMBER: 60/049911
                                                                                                                                                          40 GITCTGTCCACAGGCTCACGGCAGCCTGCTCAACCTGAAGGCCCATGGTGGAGGCCGTCACA 99
                                                                              18.9%; Score 95.6; DB 6; Length 496; 63.5%; Pred. No. 1.4e-15; tive 0; Mismatches 84; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 533, Application US/10131819A GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/056974
PRIOR PELING DATE: 1997-08-26
PRIOR PAPLICATION NUMBER: 60/059113
PRIOR PAPLICATION NUMBER: 60/059113
PRIOR PAPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR PELING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-09-17
PRIOR PAPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PAPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
               ; OTHER INFORMATION: unknown base US-10-131-813A-533
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Watanabe, Colin K
Wood, William
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Godowski, Paul J.
Gurney, Austin L.
                                                                                                                     Matches 146; Conservative
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Filvaroff, Ellen
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                                                                         Query Match
Best Local Similarity
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US-10-131-819A-533
LOCATION: 396
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Remaining Prior Application data removed - See File Wrapper or PALM.

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PRIOR APPLICATION NUMBER: 60/059117
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330NLC143
CURRENT APPLICATION NUMBER: US/10/131,823A
CURRENT FILING DATE: 2002-04-24
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18.9%; Score 95.6; DB 6; Length 496;
Best Local Similarity 63.5%; Pred. No. 1.4e-15;
Matches 146; Conservative 0; Mismatches 84; Indels (
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PRIOR APPLICATION NUMBER: 60/049911
PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-09-16
PRIOR PILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/05912
PRIOR APPLICATION NUMBER: 60/05912
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR PILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
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PRIOR PELING DATE: 1997-09-17
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Goddard, Audrey
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Gurney, Austin L.
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Filvaroff, Ellen
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 533
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                                                             TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                              NAME/KEY: unsure
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TITLE OF INVENTIÓN: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
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18.9%; Score 95.6; DB 6; Length 496;
Best Local Similarity 63.5%; Pred. No. 1.4e-15;
Matches 146; Conservative 0; Mismatches 84; Indels
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CURRENT PAPLICATION NUMBER: US/10/131,824A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR PLING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
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PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Filvaroff, Ellen
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Smith, Victoria
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                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
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            PRIOR APPLICATION UNMER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
SEQ_ID_NO 533
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18.9%; Score 95.6; DB 6; Length 496;
Best Local Similarity 63.5%; Pred. No. 1.4e-15;
Matches 146; Conservative 0; Mismatches 84; Indels (
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CURRENT APPLICATION NUMBER: US/10/131,826A
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
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PRIOR FILING DATE: 1997-09-17
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Filvaroff, Ellen
Gao, Wel-Olang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Stewart, Timothy A.
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APPLICANT: Beresini, Maureen
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Wood,William
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LOCATION: 396
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PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
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PRIOR PELLING DATE: 1997-09-17
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PRIOR PELLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PELLING DATE: 1997-09-17
PRIOR PELLING DATE: 1997-09-17
PRIOR PELLING DATE: 1997-09-18
PRIOR PELLING DATE: 1997-09-18
PRIOR PELLING DATE: 1997-09-18
PRIOR PELLING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059352
PRIOR APPLICATION NUMBER: 60/059368
PRIOR PELLING DATE: 1997-09-19
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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18.9%; Score 95.6; DB 6; Length 496;
Best Local Similarity 63.5%; Pred. No. 1.4e-15;
Matches 146; Conservative 0; Mismatches 84; Indels (
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
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Gurney, Austin L.
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LOCATION: 396
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PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
18.9%; Score 95.6; DB 6; Length 496;
Best Local Similarity 63.5%; Pred. No. 1.4e-15;
Matches 146; Conservative 0; Mismatches 84; Indels
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                           FILE KEFERENCE: E3330TALC130.
CURRENT APPLICATION NUMBER: US/10/131,829A
CURRENT FILING DATE: 2002-04-27
PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PELING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059118
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PILING DATE: 1997-09-17
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1997-09-18
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Smith, Victoria
Stewart, Timothy A.
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
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Gurney, Austin L.
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                   FILE REFERENCE: P3330R1C138
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ORGANISM: Homo Sapien
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LOCATION: 396
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US-10-125-926A-533
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PRIOR FLILING DATE: 1997-08-26

PRIOR FLILING DATE: 1997-08-18

PRIOR FLILING DATE: 1997-09-17

PRIOR PELICATION NUMBER: 60/059113

PRIOR FLILING DATE: 1997-09-17

PRIOR FLILING DATE: 1997-09-17

PRIOR FLILING DATE: 1997-09-17

PRIOR PELICATION NUMBER: 60/05912

PRIOR PELICATION NUMBER: 60/05912

PRIOR PELING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-18

PRIOR PELING DATE: 1997-09-19

PRIOR PELING DATE: 1997-09-19
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1680
CURRENT APPLICATION NUMBER: US/10/125,926A
CURRENT FILING DATE: 2002-10-15
PRIOR PILICATION NUMBER: 06/049911
PRIOR FILING DATE: 1997-06-18
PRIOR PLILICATION NUMBER: 60/056974
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Watanabe, Colin K
                                              Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapien
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February 10, 2003, 10:35:56; Search time 143 Seconds (without alignments) 757.449 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                            4569144 seqs, 644733110 residues
                                                                          OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Zb: /cgn2_6/ptcdata/1/paa/US102_COMB.pep:*
Z7: /cgn2_6/ptcdata/1/paa/US60_COMB.pep:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Ouery No. Score Match Length DB ID Description

1 957 100.0 211 27 US-09-975-456B-2 Sequence 2, Appli 3 957 100.0 211 27 US-60-203-511-2 Sequence 2, Appli 4 950 99.3 168 25 US-09-975-456B-4 Sequence 4, Appli 5 895.5 93.6 275 27 US-60-212-356-145 Sequence 145, Appli 6 892.5 93.3 248 27 US-60-212-356-180 Sequence 180, Appli 5 Page 180, Appli 180 Page 180 Page 180, Appli 180 Page 180

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US-60-229-525- US-60-229-525- US-60-229-525- US-60-234-446- US-09-975-456B- US-09-975-456B- US-09-975-456B- US-09-91-37-1 US-09-91-37-1 US-09-91-37-1 US-09-91-537-1 US-09-91-537-1 US-09-91-537-1 US-09-91-537-1 US-09-791-537-1 US-09-791-537-1 US-09-791-537-1 US-09-791-537-1 US-09-791-537-1 US-09-791-537-1 US-09-791-537-1 US-09-791-537-1 US-09-791-537-1 US-09-791-537-1 US-09-791-537-1 US-09-791-537-1 US-09-791-537-1 US-09-791-537-1 US-09-791-537-1 US-08-091-941-37 US-08-091-941-37 US-08-041-37 US-08-041-37 US-08-091-941-37 US-08-091-941-37 US-08-091-941-37 US-08-091-941-37 US-08-091-941-37 US-08-091-941-37 US-08-091-941-37 US-08-091-941-37	US-10-116-275- US-10-205-823- PCT-US00-05988- US-08-973-602- US-09-925-300- US-09-751-
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Matches 168; Conservative
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LENGTH: 168
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       61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                        61 DWCCHAHDCCYGELFDGGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNNVLC 120
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CURRENT APPLICATION NUMBER: US/60/403,468
CURRENT FILING DATE: 2002-08-14
NUMBER OF SEQ ID NOS: 6
SOFWMARE: FASLSEQ for Windows Version 4.0
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100.0%; Pred. No. 5.4e-85;
trive 0; Mismatches 0;
                                                                                                                                                                                                                                                            APPLICANT: Reddy, Kouped, APPLICANT: Yao, Monique G.
APPLICANT: Yao, Monique G.
APPLICANT: Nguyen, Danniel B.
APPLICANT: Lu, Yao,
APPLICANT: Tribouley, Catherine M.
APPLICANT: Yue, Henry
APPLICANT: Khan, Farrah A.
TITLE OF INVENTION: ILPID METABOLISM ENZYMES
TITLE OF INVENTION: ILPID METABOLISM ENZYMES
TITLE OF INVENTION: ILPID METABOLISM ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7473224CD1
                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/60/203,511
CURRENT FILLNG DATE: 200-05-11
NUMBER OF SEQ ID NOS: 4
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                                                                                                                                                                                                           ; Sequence 2, Application US/60203511
; GENERAL INFORMATION:
; APPLICANT: Das, Debopriya
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100.0%;
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Matches 168; Conservative
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CRGANISM: homosapiens
US-60-403-468-4
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LENGTH: 211
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US-60-403-468-4
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US-60-203-511-2
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SEO ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DWCCHAHDCCYGELFDGGCHPYVDHYDHTIENNTELVCSDLNKTECDKQTCMCDKNWVLC 120
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                                                    44 MKKFFTVAILAGSVLSTAHGSLINLKAMVEAVTGRSAILSFVGYGCYCGLGGRGOPKDEV 103
                                                                                                            61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
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Pred. No. 2e-84;
0; Mismatches 1; Indels (
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  0; Mismatches
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CURRENT FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
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Best Local Similarity 99.4%;
Matches 167; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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CORGANISM: Homo sapiens
US-10-104-047-3735
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TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
                  61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                      121 LMNOTYREEYRGFLNVYCOGPTPNCSIYEPPPEEV----TC-----SHQSPAPPA 166
                                                                                                                                                        Sequence 298, Application US/60229525
GBNRRAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOCATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
1 MKKFFTVALLAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
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CURRENT APPLICATION NUMBER: US/60/212,356
CURRENT FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 411
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/60/229,525
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 819
SOFTWARE: FastSEO for Windows Version 4 (
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ORGANISM: HUMAN
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LENGTH: 248
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APPLICANT: Bloomix, Inc.
APPLICANT: Bloomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: HERE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 148869
LENGTH: 168
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                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
                                                                                               61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                                                                1; Gaps
                                                                          1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
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    Score 892.5; DB 27; Length 248;
Pred. No. 1.4e-78;
2; Mismatches 6; Indels 1;
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CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 819
SOFTWARE: FastSEQ for Windows Version 4.(
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; Sequence 148869, Application US/09791537
; GENERAL INFORMATION:
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    93.3%;
94.6%;
                                    Matches 159; Conservative
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Best Local Similarity 94.6%
Matches 159; Conservative
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                     Best Local Similarity
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US-60-229-525-451
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US-60-229-525-451
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Query Match
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Pred. No. 8.8e-37;
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CURRENT APPLICATION NUMBER: US/09/969,384
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/US01/10542
PRIOR APPLICATION NUMBER: PCT/US01/10542
PRIOR PILING DATE: 2001-04-02
PRIOR PILING DATE: 2000-09-29
PRIOR PLILOR DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-40
   98.8%; Preu. no.
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                                                                                                                                81 PYVDHYDHTIENNTEIVCSD 100
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
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                        79; Conservative
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Best Local Similarity
           Best Local Similarity
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PCT-US01-10542-17
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TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION UNMER: US/60/234,446
CURRENT APPLICATION UNMER: 2000-09-18
UNMERR OF SEQ ID NOS: 1797
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GENERAL INFORMATION:
APLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 GSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCCHAHDCCYQELFDQGC 79
                                                                                                                                                             61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                             Gaps
                                                                                       1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.1%; Score 460; DB 27; Length 85;
                  78.1%; Score 747; DB 21; Length 168; 75.2%; Pred. No. 1.5e-64; tive 20; Mismatches 21; Indels (
                                                                                                                                                                                                                                                      121 IMNOTYREEYRGFINVYCQGPTPNCSIYEPPPEEVTCSHQSPAPP 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE PERERROE: CLO00772
CURRENT APPLICATION NUMBER: US/60/229,525
CURRENT FILING DATE: 2000-09-05
SUMMER OF SEO ID NOS: 819
SOFTWARE: FastSEO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 626, Application US/60234446; GENERAL INFORMATION:
                                                              Matches 124; Conservative
                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 GPTPNC 145
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SEQ ID NO 626
LENGTH: 85
                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-60-229-525-468
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APPLICANT: Human Gene Sciences, Inc.
APPLICANT: Human Gene Sequence Polynuclectides, Polypeptides, and Antibod
FITLE OF INVENTION: Human Gene Sequence Polynuclectides, Polypeptides, and Antibod
FILE REFERENCE: PT055PCT
CURRENT APPLICATION NUMBER: PCT/US01/10542
CURRENT FILING DATE: 2001-04-02
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MOOIE, et al. TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                 21 SILNIKAMVEAVTGRSAILSFVGYGGYCGLGGRGQPKDEVDWCCHAHDCCYQELFDQGCH 80
                                                                          DB 1; Length 145;
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45.5%; Pred. No. 5e-26;
tive 19; Mismatches 52; Indels
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TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM FILE REBERBRECE: 28110/35915A
CURRENT APPLICATION NUMBER: PCT/US01/12529A
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 60/197,137
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-01-17
PRIOR PLICATION NUMBER: US 09/667,298
PRIOR APPLICATION NUMBER: US 09/677,298
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-23
PRIOR FILING DATE: 2000-09-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LANBEAU, GERARD
APPLICANT: VALENTIN, EMMANUEL
TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
FITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
CURRENT APPLICATION NUMBER: US/09/975,456B
PRIOR RILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: 60/239,491
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 2.1
                                                                                                                                                                          63 CCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM 122
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                                                            8; Gaps
                                                                                    7 VAILAGSVLSTA----HGSLLNLKAMVEAVTGRSAILSFVGYGGYCGLGGRGQPKDEVDW 62
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3 LALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYMPYGCHCGLGGRGQPKDATDW 62
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3 LALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW 62
36.9%; Score 353; DB 23; Length 145; 45.5%; Pred. No. 5e-26; tive 19; Mismatches 52; Indels (
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45.5%; Pred. No. 5e-26;
tive 19; Mismatches 52; Indels {
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Matches 66; Conservative
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Matches 66; Conservative
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3 LALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYMPYGCHCGLGGRGQPKDATDW 62
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              NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.0
PRIOR FILING DATE: 2000-06-20
                                                                                                                             ORGANISM: Homo sapiens
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Sequence 80, Appl
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-188-832-80
US-10-275-998-2
PCT-USO2-29560-363
US-09-949-002-396
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US-10-131-813A-534
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Sequence 80, Application US/10188832
Sequence 80, Application US/10188832
Seguence 80, Application US/10188832
APPLICANT: Notasha
APPLICANT: AZiz, Natasha
APPLICANT: Dos Biotechnology, Inc.
APPLICANT: Dos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Bladder
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
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TITLE OF INVENTION: LIFID METABOLISM ENZYMES
FILE REFERENCE: PI-0095 USN
CURRENT APPLICATION NUMBER: US/10/275,998
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: US 01/15210
PRIOR FILING DATE: 2001-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                               TITLE OF INVENTION:
FILE REFERENCE: 018501-002330US
CURRENT APPLICATION NUMBER: US/10/188,832
CURRENT FILING DATE: 2002-011-22
PRIOR PAPLICATION NUMBER: US 60/302,814
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR PRILICATION NUMBER: US 60/343,705
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-13
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TRIBOULEY, Catherine M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10275998; GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YAO, Monique G.
NGUYEN, Danniel B.
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ELLIOTT, Vicki S.
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KHAN, Farrah A.
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Matches 168; Conservative
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        US-10-188-832-80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Gaps
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APPLICANT: MACK, David H.
APPLICANT: Wilson, Keith E.
APPLICANT: Slotulk, Albert
APPLICANT: Slotulk, Albert
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REPERENCE: 018501-002110PC
CURRENT APPLICATION NUMBER: PCT/US02/29560
CURRENT FILING DATE: 2025-11-01
PRIOR FILING DATE: 30501-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.9%; Score 353; DB 1; Length 145; 45.5%; Pred. No. 8.3e-28; tive 19; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 957; DB 6; Length 211; 100.0%; Pred. No. 6.1e-88; tive 0; Mismatches 0; Indels (
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OTHER INFORMATION: Incyte ID No: 7473224CD1
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PRIOR APPLICATION NUMBER: US 60/203,511
PRIOR APPLICATION NUMBER: US 60/207,903
PRIOR PILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: US 60/210,150
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-07
PRIOR RPLICATION NUMBER: US 60/213,392
PRIOR RPLICATION NUMBER: US 60/213,392
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 363, Application PC/TUS0229560 ; GENERAL INFORMATION:
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Matches 168; Conservative
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Gish, Kurt C.
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PCT-US02-29560-363
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PCT-US02-29560-363
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LENGIH: 145
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TYPE: PRT
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO00790
CURRENT APPLICATION NUMBER: US/09/949,002
PRIOR PILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60,221,401
PRIOR FILING DATE: 2000-09-08
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APPLICANT: AZIZ, Natasha
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Hower C.
APPLICANT: Mison, Keith E.
APPLICANT: Jotnik, Albert
APPLICANT: Zlotnik, Albert
APPLICANT: Zlotnik, Albert
APPLICANT: Jotnik, Albert
APPLICANT: BOS Biotechnology, Inc.
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer;
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer;
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer;
FILE REFERENCE: 018501-00727,003
CURRENT FILING DATE: 2001-09-13
PRIOR FILING DATE: 2001-09-20
PRIOR FILING DATE: 2001-09-20
PRIOR FILING DATE: 2001-09-20
PRIOR FILING DATE: 2001-09-20
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
63 CCQTHDCCYDHLKTQGCSIYKDYYRYNFSQG-NIHCSD-KGSWCEQQLCACDKEVAFCLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.9%; Score 353; DB 5; Length 145;
45.5%; Pred. No. 8.3e-28;
Live 19; Mismatches 52; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 10823
SOFTWARE: EastSEQ for Windows Version 4.0
SEQ ID NO 396
LENGTH: 145
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                                                 123 N--QTYREEYRGFLNVYCQGPTPNC 145
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                                                                                             121 RNLDIYOKRLRFYWRPHCRGQTPGC 145
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; GENERAL INFORMATION:
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US-09-949-002-396
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APPLICANT: USBYER, J. Craig et al.

APPLICANT: USBYER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: AND USES THEREOF

TITLE OF INVENTION: AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,002

CURRENT PILING DATE: 2000-01-28

PRIOR PILICATION NUMBER: 60/231,401

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 10823

SOFTWARE PASES OF OF WINDOWS VERSION 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/355,257
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-04-04
PRIOR PELING DATE: 2002-04-04
PRIOR PRICATION NUMBER: US 60/372,246
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 41.2
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 45.5%
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-245-882-363
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US-10-276-781-1625
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LENGTH: 145
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LENGTH: 157
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FILING DATE: 1997-09-17
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R10139
CURRENT APPLICATION NUMBER: US/10/131,813A
PRIOR PRILING DATE: 2002-04-24
PRIOR PRILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/049911
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36.8%; Score 352; DB 6; Length 14:
Best Local Similarity 45.5%; Pred. No. 1e-27;
Matches 66; Conservative 19; Mismatches 52; Indels
                               APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al.
TILE REFERENCE: 21272-018 (785 contig)
CURRENT APPLICATION NOVEL NUCLEIC Acids and Polypeptides
FILE REFERENCE: 21272-018 (785 contig)
CURRENT APPLICATION NUMBER: US/10/276,781
CURRENT FILING DATE: 2000-11-18
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1625
LENGTH: 145
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PRIOR APPLICATION NUMBER: 60/05913
PRIOR PILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
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Gerritsen, Mary E.
Goddard, Audrey
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Watanabe, Colin K
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Gurney, Austin L.
Sherwood, Steven
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APPLICANT: Beresini, Maureen
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Filvaroff, Ellen
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US-10-276-781-1625
               GENERAL INFORMATION:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C134
CURRENT APPLICATION NUMBER: US/10/131,819A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
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PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION UNBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                 Length 116;
                                                                                                                                                                                                                                                                                                                                                              Query Match 28.6%; Score 273.5; DB 6; Best Local Similarity 42.9%; Pred. No. 5.7e-20; Matches 54; Conservative 15; Mismatches 36;
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PRIOR FILING DATE: 1997.08-26
PRIOR FILING DATE: 1997.08-26
PRIOR PELING DATE: 1997.09-17
PRIOR PELING DATE: 1997.09-17
PRIOR PELING DATE: 1997.09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/05912
PRIOR FILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
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PRIOR PELING DATE: 1997-09-17
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APPLICATION NUMBER: 60/059263
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Gurney, Austin L.
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo Sapien
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Sequence 534, Application US/10131824A GENERAL INFORMATION:
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Gerritsen, Mary E.
Goddard, Audrey
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Watanabe, Colin K
Wood, William
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Filvaroff, Ellen
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                                                                                                                                                                          ; ORGANISM: Homo Sapien
US-10-131-823A-534
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US-10-131-824A-534
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C143
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                                                                                                                                                                                                                                                                                                                                   Gaps
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PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION WUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR PILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
REMBAILING PRIOR APPLICATION OF SECONDARY
NUMBER OF SECONDARY
NUMBER OF SECONDARY
                                                                                                                                                                                                                                                                                     28.6%; Score 273.5; DB 6; Length 116; 42.9%; Pred. No. 5.7e-20; tive 15; Mismatches 36; Indels 21;
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PRIOR APPLICATION NUMBER: 60/049911

PRIOR PLING DATE: 1997-06-18

PRIOR PELING DATE: 1997-06-18

PRIOR PAPLICATION NUMBER: 60/05974

PRIOR PELING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR PAPLICATION NUMBER: 60/059115

PRIOR PAPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR PELING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1997-09-18
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Smith, Victoria
Stewart, Timothy A.
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Gerritsen, Mary E.
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Wood, William
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Filvaroff, Ellen
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Matches 54; Conservative
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                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-819A-534
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APPLICANT:
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APPLICANT: Wacanadae, Colin A
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: BCERETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC126
CURRENT APPLICATION NUMBER: 06/04911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059363
PRIOR FILING DATE: 1997-09-19
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PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 534
LENGTH: 116
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28.6%; Score 273.5; DB 6; Length
Best Local Similarity 42.9%; Pred. No. 5.7e-20;
Matches 54; Conservative 15; Mismatches 36; Indels
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
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                                                                                                                                                                                                                                                                                                                                                                                                           63 CCQTHDCCYDHLKTQGCGIYKDN-----NKSSIHCMDLSQRYC------LMAVF 105
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PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
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PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-06-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
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PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
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Stewart, Timothy A.
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Gerritsen,Mary E.
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Wood,William
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Gurney, Austin L.
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                                                                                                                              ORGANISM: Homo Sapien
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US-10-131-824A-534
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US-10-131-826A-534
                                                                SEQ ID NO 534
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63 CCQTHDCCYDHLKTQGCGIYKDN-----NKSSIHCMDLSQRYC-------LMAVF 105
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C138
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                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 550
                                                                                                                                                             28.6%; Score 273.5; DB 6; Length 116; 42.9%; Pred. No. 5.7e-20; ive 15; Mismatches 36; Indels 21.
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CURRENT FILING DATE: 2002-04-27
PRIOR PAPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-26
PRIOR PILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
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PRIOR FILING DATE: 1997-09-17
PRIOR PELLING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PAPLICATION NUMBER: 60/059263
PRIOR PAPLICATION NUMBER: 60/059263
PRIOR PELING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
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PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
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Wood, William
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Gerritsen,Mary E.
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DeForge, Laura
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Gurney, Austin L.
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Filvaroff, Ellen
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NUMBER OF SEQ ID NOS: 550
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                                                                 TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                Best Local Similarity
Matches 54; Conserv
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                   SEQ ID NO 534
LENGTH: 116
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PRIOR ELLING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR PLING DATE: 1997-09-17
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CURRENT APPLICATION NUMBER: US/10/125,926A
CURRENT FILLING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
Wood, William
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Gerritsen, Mary E.
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Filvaroff, Ellen
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                                         ORGANISM: Homo Sapten
US-10-131-829A-534
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Best Local Similarity
Matches 54; Conserva
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CORGANISM: Homo Sapien

US-10-125-926A-534

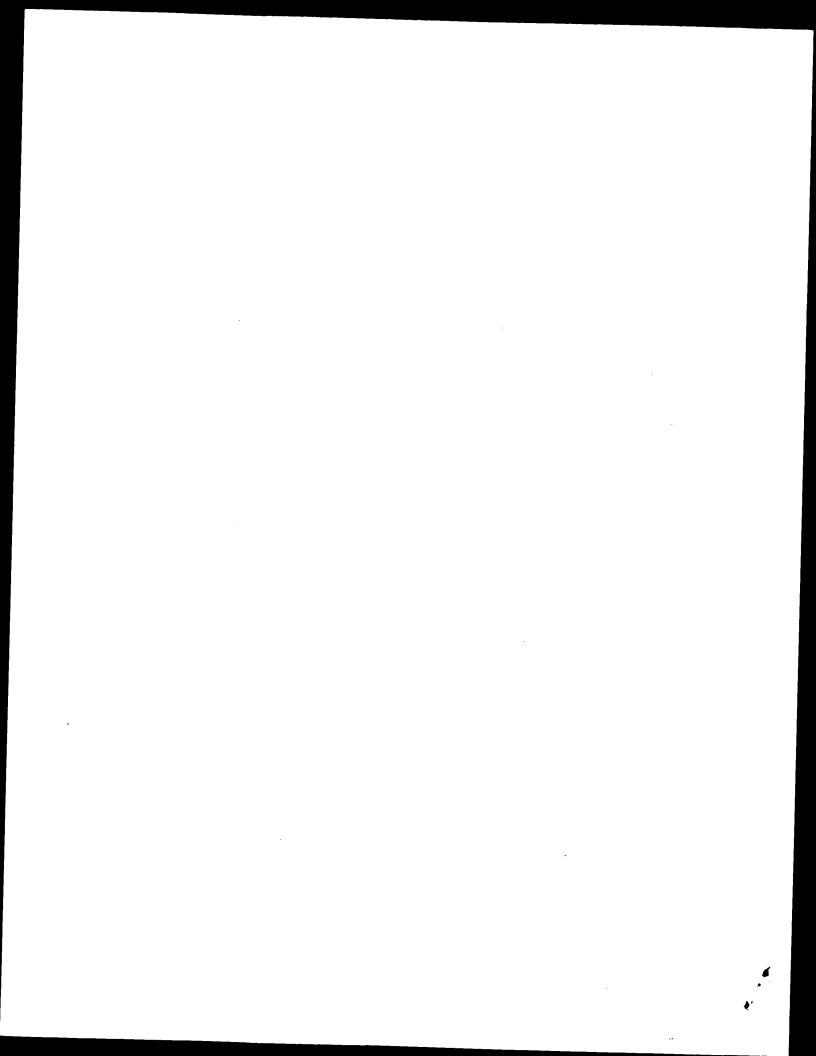
28.6%; Score 273.5; DB 6; Length 116;

Query Match

Best Local Similarity 42.9%; Pred. No. 5.7e-20;

Best Local Similarity 42.9%; Pred. No. 6.7e-20;

Best Local Similarity 42.9%; Pred. No.
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2003, 00:10:29; Search time 2609 Seconds

(without alignments)
5655.470 Million cell updates/sec

Title: US-09-975-456B-1
Sequence: 507
Sequence: 1 atgaagaagttcttcaccgt.......cgccccccgcccctcctag 507
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES ID	, ., ., .,	AF1660 HS340N1	AL1581	AL8441 AC1180	AC1061	AF1129 AF1886	BC0257	AX454400	BC029	AC1180	AR1983	RRU0779	AF16271	MMU6687	RRU03	AR081995	AR1983	E3/214 AF11298	AF1694	AF16940	E37202	AF1243	AR198392	HSU0309	AK09769	AR10591	AR21135	050705B	AF18927	BD0101	AL15817	TMPHA2N	⋖ :	ACU2133
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ALIGNMENTS

AF306566 507 bp mRNA linear PRI 18-JAN-2001 Homo sapiens group IIF secreted phospholipase A2 mRNA, complete	AF306566.1 GI:12276059	piens.	Eukkaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 507)	Valentin,E., Singer,A.G., Ghomashchl,F., Lazdunski,M., Gelb,M.H. and Lambeau,G.
AF306566 Homo sapie cds.	AF306566 AF306566.1	Homo sapiens. Homo sapiens	Eukaryota; Mammalia; 1 (bases	Valentin, E., S. and Lambeau, G.
RESULT 1 AF306566 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE ORGANISM		AUTHORS

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Yue, H., Khan, F.A., Gandhi, A.R., Au-You
Elliott, V.S., Ding, L. and Thornton, M.
Lipid metabolism enzymes
Patent: WO 0185956-A 7 15-NOV-2001;
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/db_xref="taxon:9606"
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GCYCGLGGRGQPKDEVDWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLN
KTECDKQTCMCDKNMVLCLMNQTYREEYRGFLNVYCQGPTPNCSIYEPPPEEVTCSHQ
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                                                                                                    Submitted (18-SEP-2000) IPMC, CNRS, 660, Route des Lucioles Sophia Antipolis, Valbonne 06560, France
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/protein_id="AAG50242.1"
/db_xref="G1:12276060"
             phospholipase A(2)
Biochem. Biophys. Res. Commun. 279 (1), 223-228 (2000)
20563827
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Direct Submission
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                                                                                        Au-Young, J., Lal, P., Kearney, L.,
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                                                                Das, D., Reddy, R., Yao, M.G., Nguyen, D.B., Lu, Y., Tribouley, C.M.,
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                                                                                  Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K., Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Irie, R., Ctsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kande, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Sugiyama, A., and Isogai, T., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K., Nabo, human, CDNA sequencing project
                                                                                                                                                                                                                                                                                                                           Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa Kamatari, Kisarazu, Chiba 292-0812, Japan
RE-mail:genomicséhri.co.jp, Tel:81-438-52-395, Fax:81-438-52-3986)
REDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: construction: Helix Research Institute (HRI); cupported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: Key Technology Center, National Institute of Technology and Nauation; clone selection for full insert sequencing: RAB, Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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GCYCGLGGRGQPKDEVDWCCHAHDCCYQELFDQGCHPYVDHYDHTIBNNTEIVCSDLN
KTECDKQTCMCDKNMVLCLANOTYREEYRGFLNVYCQGPTPNCSIYGPPPEEVTCSHQ
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="G1:21752562"
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/clone="THYMU2005576"
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Isogai,T. and Yamamoto,J.
Direct Submission
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clone: THYMU2005576
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Matches 506; Conservative
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                   Homo sapiens
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases I to 906) 1 (valentin, E., Ghomashchi, F., Gelb, M.H., Lazdunski, M. and Lambeau, G. On the diversity of secreted phospholipases A(2). Cloning, tissue distribution, and functional expression of two novel mouse group II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROD 02-NOV-1999
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GCYCGLGGRGHPMDEVDWCCHAHDCCYEKLFEQGCRPYVDHYDHRIENOTMIVCTELN
ETECDKQTCECDKSLTLCLKDHPYRNKYRGYFNVYCQGPTPNCSIYDPYPEEVTCGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 906)
Valentin, E., Ghomashchi, F., Gelb, M.H., Lazdunski, M. and Lambeau, G.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (07-JUL-1999) IPMC, CNRS, 660, route des Lucioles, Valbonne 06560, France 3 (bases 1 to 906)
Valentin, E., Ghomashchi, F., Gelb, M.H., Lazdunski, M. and Lambeau, G. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF166099 906 bp mRNA linear ROD 02-NOV-19
Mus musculus group IIF secreted phospholipase A2 (Pla2g2f) mRNA,
                                                                                                                                                                                         301 CTCAACAAGACAGAGTGTGACAAGCAGACATGCATGTGACAAGAACATGGTTCTGTGC 360
                         361 CTCATGAACCAGACGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCCAGGGC 420
                                                                                                                        Submitted (02-NOV-1999) IPMC, CNRS, 660, route des Lucioles, Valbonne 06560, France Sequence update by submitter On Nov 2, 1999 this sequence version replaced g1:6164699.
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Pred. No. 3.3e-66;
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/db_xref="G1:6174881"
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                                                                                                                                                                                                                                                                                          481 TCCCCAGCGCCCCCGCCCTCCCTAG 507
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/EC_number="3.1.1.4"
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251. .757
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14661. 14727
/note="Harlequin repeat: matches 6829. .6895 of consensus"
14731. .14896
/note="LTR2 repeat: matches 5. .160 of consensus"
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Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
/product="dJ340N1.1 (novel phospholipase similar to mouse
/pospholipase A2 group IIF (PLA2G2F))"
/protein_id="GA012707.1"
/db_xref="G1:10697037"
                                                                                                                                                                                                                                                                                                       IMPORTANT: This sequence is not the entire insert of clone RP3-340N1 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP4-745EB is at 13546B in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="continues in dJ169023 (AL158172), gene dJ169023.4
                                                                                                                                                                     http://www.sanger.ac.uk/HGP/Chrl
RP3-340N1 is from the library RPCI-3 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
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/note="HERVE repeat: matches 5915. .6005 of consensus"
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/note="LTR2 repeat: matches 266. .384 of consensus"

15013. 1109

/note="LTR2 repeat: matches 353. .449 of consensus"

complement(16791. .17143)

/note="match: GSS: Em:AQ279224"

18790. .18933

/note="9 copies 16 mer 72% conserved"

18791. .18936

/note="73 copies 2 mer gt 74% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8456. .8587

//note="LTR2 repeat: matches 1. .125 of consensus"

8636. .8819

/note="LTR2 repeat: matches 266. .448 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="Alu repeat: matches 2. .78 of consensus"
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/note="2 copies 94 mer 95% conserved"

4003. .4078

/note="2 copies 38 mer 89% conserved"

6385. .6791

/note="match: GSS: Em:AQ007442"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(3608. .4002)
/note="match: GSS: Em:B90571"
complement(3643. .4002)
/note="match: GSS: Em:AQ085265"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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/gene="dJ340N1.1"
<2689. .2900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission

Submitted (04-007-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

on Mar 12, 1998 this sequence version replaced gi:2578090.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HS340N1 135571 bp DNA linear PRI 05-OCT-2000 Human DNA sequence from clone RP3-340N1 on chromosome 1p35-36.2 Contains the 3' part of a gene for a novel phospholipase similar to mouse phospholipase A2 group IIF (PLA2G2F), complete sequence. 298257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 135571)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 CTCATGAACCAGACGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCCAGGGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCACGCCCAACTGCAGCATCTATGAACCGCCCCTGAGGAGGTCACCTGCAGTCACCAA 480
                                                                                                                                                                                                                                                                                                                               241 CCCTATGTGGACCACTATGATCACACCATCGAGAACAACACTGAGATAGTCTGCAGTGAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           611 CICAAGGAICACCCATACAGGAACAAGIACCGAGGCTACTICAACGICTACTGCCAGGGC 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AGCCIGCICAACCIGAAGGCCAIGGIGGAGGCCGICACAGGGAGGAGGGCCCAICCIGICC 120
                                                                                                                                                                                                                   121 TTCGTGGGCTACGGTTGCTACTGTGGGCGGGGGGCCCGTGGCCAGCCCAAGGATGAGGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    490
                                                                           1 ATGAAGAAGTICTICACCGIGGCCAICCTIGCIGGCAGCGITCTGTCCACAGCICACGGC 60
                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             181 GACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAACTCTTTGACCAAGGCTGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                301 CICAACAAGACAGAGTGTGACAAGCAGACATGCATGTGTGACAAGAACATGGTTCTGTGC
                             0; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 TCCCCAGCGCCCCCCCCCTCCCTAG 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                731 CTCCCTGCGACCCCTGTCTCAACCTAG 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; phospholipase; PLA2G2F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z98257.1 GI:2956660
                                     Matches 403; Conservative
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DEFINITION

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HS340N1

ACCESSION

KEYWORDS

/ERSION SOURCE ORGANISM

JOURNAL

COMMENT

REFERENCE AUTHORS

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/note="MER45B repeat: matches 975. .1039 of consensus" 30193. .3026 /note="LIMC/D repeat: matches 5706. .5775 of consensus" complement(31785. .32194)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comptement(31785, 31194)

// note="match: GSS: Em:AQ277413"
32909, 33153
33499, .3361
// note="LTR16A repeat: matches 121, .295 of consensus"
33695, .33801
// note="LTR16A repeat: matches 121, .295 of consensus"
33705, .33804
// note="1" copies 16 mer 64% conserved"
3705, .33894
// note="5" copies 38 mer 66% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 5600. .5876 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44473. ...4664
/note="MERSB repeat: matches 1. .198 of consensus"
complement(45904. .46320)
/note="match: STS: Em. AA394141"
complement(45950. .46366)
/note="match: STS: Em. T86344"
complement(46154. .46576)
/note="match: GSS: Em. AQ340310"
complement(48597. .49196)
/note="match: STS: Em: AA35547"
52724. .53004
/note="LJMC1 repeat: matches 5600. .5876 of consensus"
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86860. .87858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MER11A repeat: matches 1. .1266 of consensus"
                                                                                                                                                                                                                                                                                                                                                   20107. 29271
Note="MER45 repeat: matches 1. .178 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63305. .63419
/note="FLAM_C repeat: matches 2. .119 of consensus"
67470. .67491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61040. .61202
/note="FRAM repeat: matches 2. .162 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="102 copies 2 mer tg 62% conserved"
                                                                                                                                                                       /note="22 copies 2 mer tg 81% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33712. .33867
/note="78 copies 2 mer tg 64% conserved"
33898. .34201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34208. .34321
/hote="57 copies 2 mer tg 69% conserved"
34235. .34330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="11 copies 2 mer aa 100% conserved"
32874. .83099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34205. 34205. ... 4 wer tg 62% conservante de conservante de conserved de conserved
18810. .18923
/note="3 copies 38 mer 77% conserved"
20154. .20297
                                                                                                /note="9 copies 16 mer 72% conserved"
20297, .20340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="8 copies 38 mer 60% conserved" 3991. .34194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="6 copies 16 mer 71% conserved" 36684. .37082
                                                                                                                                                                                                         25520. .25869
/note="match: GSS: Em:AQ225965"
                                                                                                                                                                                                                                                                                   25529. .25754
/note="match: GSS: Em:B58996"
29107. .29271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence-not_experimental
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/note="CpG island"
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                                                                                                                                                                                                                                                                                                                             | Mode="MER4D repeat: matches 388. .451 Of consensus" |
| Mode="MER4D repeat: matches 451. .1015 of consensus" |
| Mode="MER81 repeat: matches 1. .114 of consensus" |
| Mode="MER81 repeat: matches 1. .114 of consensus" |
| Mode="MSTD repeat: matches 313. .394 of consensus" |
| Mode="MSTD repeat: matches 1. .317 of consensus" |
| Mode="MSTC repeat: matches 1. .317 of consensus" |
| Mode="MSTC repeat: matches 1. .328 of consensus" |
| Mode="MSTR41A repeat: matches 1. .328 of consensus" |
| Mode="LiP87 repeat: matches 5960. .6141 of consensus" |
| Mode="LiP87 repeat: matches 5960. .6141 of consensus" |
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98743 bp DNA linear PRI 25-OCT-200
Human DNA sequence from clone RP1-169023 on chromosome 1 Contains
ESTS, STSS and GSSS. Contains the PLA2GS gene for two isoforms of
phospholiapse A2 group V, a novel gene, the PLA2GSD gene for
phospholiapse ginnilar to mouse phospholipase A2 group IID and the 5' part of the gene for
phospholiapse similar to mouse phospholipase A2 group IIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 [bases 1 to 98743)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2689 GTGACCTCAACAAGACAGAGTGTGAGAAGAGAGAGAGAGTGTGACAAGAAGATGCGTTC 2748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2809 AGGCCCCCACGCCCAACTGCAGCATCTATGAACCGCCCCTGAGGAGGTCACCTGCAGTC 2868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 GTGACCTCAACAAGACAGGGGGTGTGACAAGCAGGAAGATGCATGTGTGACAAGAACATGGTTC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 TGTGCCTCATGAACCAGACGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER41A repeat: matches 316. .554 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                416 AGGCCCCACGCCCAACTGCAGCATCTATGAACCGCCCCTGAGGAGGTCACCTGCAGTC 475
                                                                                           73468. .93679
//note="MRR4B repeat: matches 3. .175 of consensus"
//note="MRR4B repeat: matches 175. .212 of consensus"
//note="MRR4B repeat: matches 175. .212 of consensus"
//note="MRR4D repeat: matches 388. .451 of consensus"
//note="MRR4D repeat: matches 388. .451 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
91919. .92837
/note="wER49 repeat: matches 7. .923 of consensus"
93468. .93679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 212; DB 9; Length 135571; Pred. No. 1.7e-37;
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Matches 212; Conservative
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INPOGRANT: This sequence is not the entire insert of clone RR1-169023 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RR1-169023 is at 1 in this sequence. The true left end of clone RR1-169023 is at 1 in this sequence. It is contined to the contined of clone RR1-169023 is at 1 in this sequence.
                                                                                                                                                                      The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/mgy/Chrl
RPI-169023 is from the library RPCI-1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3337. .6694 note="LIMC4 repeat: matches 6189. .6548 of consensus"
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/note="LIM4 repeat: matches 5497. .5798 of consensus"
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/note="MLT1E repeat: matches 507. .567 of consensus"
7800. .8099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          781. .909
/note="MER65-internal repeat: matches 1665. .1801 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    630. .756
/note="MER83-internal repeat: matches 1668. .1825 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    866. .6336
hote="MER4A2 repeat: matches 1. .504 of consensus"
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note="MER4-internal repeat: matches 3840. .6087 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           928. .1655
/note="MER4-internal repeat: matches 1764. .2472 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                593. .2950
note="THEIB repeat: matches 1. .364 of consensus"
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/note="LTR8 repeat: matches 1. .257 of consensus"
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/db_xref="taxon:9606"
/chromosome="1"
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/note="match: STS: Em
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/clone_lib="RPCI-1"
107. .371
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2593. .2950
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/gene="di169023.2" .44308)
/gene="di169023.2" .44308)
/gene="di169023.2" .44308)
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join(12774. .12834,16626. .16744,22015. .22080,44003. .44308)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      700199. 19511.
/note="LlMC2 repeat: matches 5204. .5592 of consensus"
19567. 19724
                                                                                                                                                                                    /note="LiPA13 repeat: matches -651. .-544 of consensus" 9520. 10539
/note="LiM4 repeat: matches 2963. .3988 of consensus" 10553. 10664
/note="LiM4 repeat: matches 2243. .2357 of consensus" 10665. .10936
                                                                                                                                9244. 9359
/note="ilMCl repeat: matches 6210. 6327 of consensus"
9376. 9483
                                                                                                                                                                                                                                                                                                                         //note="LiN4 repeat: matches 2230. .2244 of consensus" 10939. .11702 //note="LiNEC repeat: matches 2206. .2980 of consensus" 112333. .12282 //note="Alux repeat: matches 251. .302 of consensus" 12293. .12588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mote="5" UTR probably continues in bA66M4 (AL360079)
3rd exon misses correct 3' splice site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Alusx repeat: matches 1. .309 of consensus" 17754. .17885
/note="FLAM_C repeat: matches 1. .132 of consensus" complement(17768. .18077)
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                                                                             note="L2_repeat: matches 2537, .2705 of consensus"
                                                                                                    8984. 9131
/note="L2 repeat: matches 2414. 2576 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
13384. .13694
/note="Alusx repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                                                                                             /translation="MSMPLIQKPEGTHSPLRPSPTQQSQESDSGHRTW"
17434. 17743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="dJ169023.2.1 (novel protein)"
/note="match: ESTs: Em:AA402475 Em:AA293827"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
/product="di56023.2.1 (novel protein)"
/protein.id="CAC13157.1"
/db_xref="G1:10862734"
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         /note="match: GSS: Em:AQ263839"
complement(8044. .8537)
                           complement(8044. .8537)
/note="match: GSS: Em:AQ591805"
complement(7990.
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1. .9080
/note="assembly_fragment:01559
fragment_chain:1
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//otce=assembly_fragment:01433
fragment_chain:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81857. .88238
/note="assembly_fragment:01233
fragment_chain:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="assembly_fragment:01964
fragment_chain:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
                      Chemistry: Dye-terminator; 100% of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP23-352K10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib-"RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3005; gap of 88238;
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13836 21719; cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_end:T7
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                                                                                                                                                                                                                                                                                                                                             22116. .22295
//note="LiMa repeat: matches 5319. .5503 of consensus"
//note="LiMa repeat: matches 5319. .5503 of consensus"
//note="match: GSS: Em:AQ743836"
22535. .22832
//note="Alubra repeat: matches 3. .312 of consensus"
//note="LiMc4 repeat: matches 7505. .7702 of consensus"
//note="LiMc4 repeat: matches 7505. .7702 of consensus"
//note="LiMc4 repeat: matches 7505. .39369, join(23487. .23607,29903. .29956,37963. .38012,39225. .39369,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Luold DNA linear HTG 17-JUL-2002 PROGRESS ***, 12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-7UL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
20141. .20440
/note="AluJb repeat: matches 2. .297 of consensus"
20411. .20476
/note="AluJo repeat: matches 265. .301 of consensus"
20531. .20547
/note="LIM4 repeat: matches 4735. .4751 of consensus"
                                                                                                                                                                                                            /note="Alusgrapeat: matches 1. .306 of consensus"
21284. .21593
/note="LIM4 repeat: matches 4891. .5163 of consensus"
21594. .21892
/note="Alusp repeat: matches 1. .301 of consensus"
21893. .21968
/note="LIM4 repeat: matches 5163. .5242 of consensus"
                                                                                                                                                         20845. .20978
/note="LiM4 repeat: matches 4751. .4891 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 GITCIGICCACAGCICACGGCAGCCIGCICAACCIGAAGGCCAIGGIGGAGGCCGICACA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                20548. .20844
/note="AluSx repeat: matches 1. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.2%; Score 148; DB 9; Length 98743; 100.0%; Pred. No. 4e-23; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: XGAA4, Version 4.5
Sequencing vector: M13; M77815; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: humguery@eanger.ac.uk
Project Information
Center project name: bM352K10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----- Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 GGCCAGCCCAAGGATGAGGTGGACTGGT 187
                                                                                                                                                                                                20979. .21283
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HTG; HTGS_PHASE1.
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LOCUS
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Consensus quality: 187736 bases at least Q40 consensus quality: 18824 bases at least Q30 consensus quality: 184523 bases at least Q30 Insert size: 185489; sum-of-contigs Insert size: 183886; S.4% error; agarcae-fp Quality coverage: 5.6% in Q20 bases; sum-of-contigs coverage: 5.87x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46102: gap of 100 bp 58259: contig of 12157 bp in length 58359: gap of 100 bp 72342: contig of 13983 bp in length 72442: gap of 100 bp 100 bp 1156: contig of 9314 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88239 88338: gap of 100 bp 88339 107178: contig of 18840 bp in length 107179 107278: gap of 100 bp 107279 159991: contig of 52713 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p of 100 bp contig of 24183 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9080: contig of 9080 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9081 9180: gap of 100 bp 9181 13735: contig of 4555 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 100 bp contig of 7884 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of 6382 bp in length
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fragment_chain:1"
13836. .21719
/note="assembly_fragment:00382
fragment_chain:1"
21820. .46002
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//orte="assembly_fragment:00345
fragment_chain:1"
46103. .58259
//orte="assembly_fragment:00824
fragment_chain:2"
88360. .72342
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus clone CH230-117D17, *** SEQUENCING IN PROGRESS ***, 74 unordered pieces. AC118094
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 GIGCCICAIGAACCAGACGIACCGAGAGGAGIACCGIGGCIICCICAAIGICIACIGCCA 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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47647 a 45898 c 45957 g 45956 t 1131 others
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                                                                                           /note="assembly_fragment:00877
fragment_chain:2"
160092. 175174
/note="assembly_fragment:01936
fragment_chain:2"
17527s. 186589
/note="assembly_fragment:00819
fragment_chain:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.8%; Score 135.8; DB 2 77.7%; Pred. No. 2.1e-20; Live 0; Mismatches 47
                   /note="assembly_fragment:00095
fragment_chain:2"
107279. 159991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 50976 TGGCCTCCCTGCGACCCTGTCTCAACCTAG 50946
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HTG; HTGS_PHASE1.
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88339. .107178
                                                                                                                                                                                                                                                                                                                         clone_end:SP6
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Best Local Similarity
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Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J. Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Ma,J., Mabeshwari,M., Mapua,P., Martin,R., Martindale,A., Mattinez,E., Mawhiney,E., McLeod,M.P., Medor,M., Mei,G., Merzker,M., Miner,G., Micchell,T., Mohabbat,K., Morgan,M., Morris,S., Moyer,M., Newtson,N., Nguyen,N., Nguyen,N., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oraqunys,N., Ovledo,R., Pare,R., Patton,B., Peery,J., Perez,L., Pitckens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Retves,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Stone,H., Tansey,J., Taylor,C., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Talefrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,O., Williamson,A., Wilczyk,R., Wooden,S., Worley,K., Weinston,S., Worley,K., Weinston,D., Weinston,D.,
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NOTE: This is a 'working draft' sequence. It currently consists of 74 contigs. The true order of the pleces arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (13-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 157317)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Worley,K.C.
Direct Submission
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department Colonicular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jul 14, 2002 this sequence version replaced gi:20258206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 consensus quality: 98821 bases at least Q40 consensus quality: 107462 bases at least Q30 consensus quality: 113497 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
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I (bases 1 to 176574)

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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 GTGCCTCATGAACCAGACGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCCA 416
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Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homes,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Karlsson,E., Kally,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Martinez,E.,
Mansey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mowtson,M., Moygan,M., Morris,S.,
Miner,G., Miner,S., Newtson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nackerson,E., Nwokenkwo,S., Oguh,M., Okwuon,G.,
Oragunye,N., Ortedo,R., Pace,A., Payton,B., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Stoson,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,R., Tamerisa,R., Tang,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,R., Tamerisa,R., Tang,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,R., Tang,H.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watligton,S.,
Walliams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Whilliams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Whilliams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.cdu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 176574)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jul 11, 2002 this sequence version replaced gi:18138623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Blg Dye: 100% of reads
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Consensus quality: 121890 bases at least Q40
Consensus quality: 126967 bases at least Q30
Consensus quality: 131259 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
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Direct Submission
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COMMENT

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Ishizaki,J. Suzuki,N., Higashino,K., Yokota,Y., Ono,T., Kawamoto,K., Fujii,N., Arita,H. and Hanasaki,K. Cloning and characterization of novel mouse and human secretory bhospholipase A(2)s
J. BJOL. Chem. 274 (35), 24973-24979 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGCCTCATGAACCAGACGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCCA 416
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Ishizaki,J., Suzuki,N., Higashino,K. and Hanasaki,K.
Direct Submission
Submitted (11-DEC-1998) Shionogi Research Laboratories,
Fukushima-ku, Sagisu 5-12-4, Osaka 553-0002, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 129.4; DB 2; Length 1
Pred. No. 5.7e-19;
0; Mismatches 51; Indels
                      bp in length
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gap of unknown length
contig of 3434 bp in length
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gap of unknown
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gap of unknown
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Matches 160; Conservative
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/translation="melalicglyvmagviploggilnlnkmykovygkmpilsympy GCHCGLGGRGOPKDATDWCCQTHDCCYDHLKTOGCGIIYDDYRRYNFSQGNIHCSDKGS WCEQQLCACDKEVAFCLKRNLDTYQKRLRFYMRPHCRGQTPGC"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1938)
Shakhov,A.N., Rubtsov,A.V., Lyakhov,I.G., Tumanov,A.V. and
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SPLASH (PLAZIID), a novel member of phospholipase A2 family, is associated with lymphotoxin deficiency Genes Immun. 1 (3), 191-199 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   /note="results in glycine to serine substitution"
/replace="a"
257 c 238 g 177 t
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Shakhov,A.N., Rubtsov,A.V., Lyakhov,I.G., Tumanov,A.V. and
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                                                                                                                                                                                                        /product="group IID secretory phospholipase A2"
/protein_id="AAD51390.1"
/db_xreff="G1:5771420"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 19.5%; Score 99; DB 9; Length 878; Best Local Similarity 57.2%; Pred. No. 5.1e-12; Matches 202; Conservative 0; Mismatches 145; Indels
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/organism="Homo sapiens"/db_xref="taxon:9606"
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                                                                                                                               /qene="PLA2"
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                                                                                                                                                                                                                                                                                                                                                                        /translation="MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPY
GCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGCSIYKDYYRYNFSQGNIHCSDKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;;
                                                                                                                                                                                                                                                                            /note="PLA2IID; similar to Mus musculus phospholipase A2"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2747)
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Submitted (06-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
                        Direct Submission
Submitted (20-SEP-1999) Laboratory of Molecular Immunoregulation,
IRSP, SAIC, NOI-FORDC, P.O. Box B, Frederick, MD 21702, USA
Location/Qualifiers
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Pred. No. 4.9e-12;
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                                                                                                                                                                                                                                                                                                             /product="phospholipase A2"
/protein_id="AAF09020.1"
/db_xref="GI:6453793"
                                                                                                                        /organism="Homo sapiens"
                                                                                                                                        /db_xref="taxon:9606"
                                                                                                                                                            /chromosome="1"
/map="1q35"
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                                                                                                                                                                                                                                                          /gene="SPLASH"
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                                                                                                                                                                                                                     /gene="SPLASH"
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        Nedospasov, S.A.
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KEYWORDS
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Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.W.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.E., Touchman,M. Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRK Plate: 49 Row: m Column: 9 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6912595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="melallcglvvwagviploggilnlnkwvkqvyckwpllsywpy gchcelcgrgopkDappwccophDccyDHLKTQGCSIYkDYYRYNFSQGNIHCSDKGS WCEQQLCACDKEVAFCLKRNLDTYQKRLRFYWRPHCRGQTPGC"

762 c 668 g 598 t
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                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="MGC:34386 IMAGE:5223912"
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Pred. No. 4.8e-12;
0; Mismatches 145; Indels
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/protein_id="AAH25706.1"
/db_xref="G1:19344001"
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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Mus musculus testis-specific low molecular weight phospholipase A2
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1445)
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                        Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E., Gao, N.O., Geritleen, M. E., Goddard, A., Godowski, P.J., Gurney, A.L., Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K., Wood, W.L. and Zhang, Z.
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Tischfield,J.A.
Localization of group IIc low molecular weight phospholipase A2
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Novel group V phospholipase A2 involved in arachidonic acid
mobilization in murine P388D1 macrophages
J. Biol. Chem. 271 (50), 32381-32384 (1996)
97113049
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                                        linear
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Pred. No. 3.1e-11
0; Mismatches 84
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                                      AX464400
Sequence 533 from Patent WO0140466.
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/db_xref="taxon:9606"
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Location/Qualifiers
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Matches 146; Conservative
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/evidence-experimental
/product-"phospholipase A2"
/protein_id="AAC52936.1"
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GCYGGLGGKGLPVDATDRCGWAHDCCYHKLKFYGCQPILNAYQFTIVNGTVTCGCTVA
SSCPCGGRACECDKQSYYCFKENNLAYYEKAFKQLFPTRPQCGRDKLQC"
388 g 312 t
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Strausberg, R.
                                                                                                                           Direct Submission
Submitted (05-DEC-1994) Jay A. Tischfield, Medical and Molecular
Genetics, Indiana University School of Medicine, 975 W. Walnut,
Indianapolis, IN 46202, USA
Location/Qualifiers
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Mus musculus, Similar to phospholipase A2, group IIC, clone MGC:18412 IMAGE:4234596, mRNA, complete cds.
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Pred. No. 1e-10;
mRNA to meiotic cells in the mouse J. Cell. Biochem. 64 (3), 369-375 (1997) 97209919
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179. .631
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Best Local Similarity 56.4%;
Matches 195; Conservative
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Tischfield, J.A.
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SSCLCGQRACECDKQSVYCFKENLATYEKAFKQLFPTRPQCGRDKLQC"
a 386 c 390 g 319 t
                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) modepaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 25 Row: j Column: 23 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6679366.
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NIH-MGC Project URL: http://mgc.nci.nih.gov
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198. .650
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Human libid metabo	Human phospholipas	Human cDNA encodin	Human secretory ph	Human EST-derived	Human protein enco	Human CG95 (or C87	Human PRO1561 cDNA	Human cDNA sequenc
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			re Match Length DB]	2270	592	854	878	1927	1927	1931	496	496
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The sequence encodes a novel human lipid metabolism enzyme (LME-2) of the invention. The invention relates to novel human LME's, and the polymucleotides which identify and encode them. The enzymes of the invention have cytostatic, neuroprotective, immunosuppressive, anti-inflammatory, and cardiovascular activity. The polypeptides and polymucleotides have a use in gene therapy and enzyme therapy. The lipid metabolism enzymes are useful in the diagnosis, treatment and prevention of cancer, neurological disorders, autoimmune/inflammatory disorders, and cardiovascular disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of lipid metabolism enzymes. LMEs may also be used to screen for compounds that modulate the activity of LME. Polymucleotides encoding LME may be used for sometic or germline gene therapy, to detect and quantify gene expression in biopsied tissues in which expression of LME may be correlated with disease, to generate a transcript image of a tissue or cell type, to generate hybridization probes useful in mapping the naturally occurring genomic sequence, and for screening libraries of compounds in drug screening techniques. The polypeptide sequences may be used to analyse the proteome of a tissue or cell type. Oligonucleotide primers derived from polynucleotide sequences encoding LME may be used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 CCCACGCCCAACTGCAGCATCTATGAACCGCCCCTGAGGAGGTCACCTGCAGTCACCAA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCATGAACCAGACGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCTACTGCCAGGGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGAAGAAGTTCTTCACCGTGGCCATCCTTGCTGGCAGCGTTCTGTCCACAGGTCACGGC 60
                                                              Yue H;
                                                              Lu Y, Tribouley CM, Yue H, P, Kearney L, Elliott VS;
                                                                                                                                                                                                                                                                                       New lipid metabolism enzymes useful for diagnosing, treating and preventing cancer, neurological disorders, autoimmune/inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCAACAAGACAGAGTGTGACAAGCAGACATGCATGTGTGACAAGAACATGGTTCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 507; DB 24; Length 2270; Best Local Similarity 100.0%; Pred. No. 3.7e-119; Matches 507; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2270 BP; 476 A; 690 C; 709 G; 395 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                     disorders, and cardiovascular disorders
                                                              Yao MG, Nguyen DB,
AR, Au-young J, Lal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detect single nucleotide polymorphisms.
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 118-119; 122pp; English.
(INCY-) INCYTE GENOMICS INC.
                                                              Reddy R, Yao
, Gandhi AR,
                                                                                                                      Thornton M;
                                                                                                                                                                                        WPI; 2002-089794/12.
                                                                                                                                                                                                                        P-PSDB; ABB08202
                                                                                                  FA,
                                                                                                                                Ding L,
                                                              Das D,
                                                                                                  Khan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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The present sequence is the coding sequence of human phospholipase I (HPPLI): The protein produced from this sequence is involved in the hydrolysis of membrane phospholipids. The protein and its coding sequence can be used to diagnose and treat the following: cancers such as prostate, breast and testicular cancers, autoimmune and inflammatory disorders such as AIDS, allergies, anaemia, asthma, atherosclerosis, crohn's disease, diabetes mellitus, emphysema, Graves disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, psoriasis, rheumatoid arthritis and systemic lupus erythematosus, infection caused by viruses, fungi, bacteria, parasites and protozoa, and reproductive disorders including infertility, disruptions of the menstrual cycle,
Human phospholipase genes and proteins useful to diagnose, prevent or treat cancer, autoimmune or inflammatory or reproductive disorders
                                                                                                                                                                                                                                                  Human; phospholipase 1; HPPL1; cancer; autoimmune disorder; inflammatory disorder; reproductive disorder; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= c
/note= "this is a putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                      /note= "this is a putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= d
/note= "this is a putative mature HPPL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "this is a putative mature HPPL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guegler KJ, Corley NC,
                                                                                                                                                                                                                        Human phospholipase 1 HPPL1 coding sequence.
                                                        TCCCCAGCGCCCCCCCCTCCTAG 728
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
29..466
                                                                                                                                                                                                                                                                                                                                                           /product= "HPPL1"
29..91
                                         TCCCCAGCCCCCCCCCCCTCCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 74; 80pp; English.
                                                                                                                                       BP.
                                                                                                                                       AAA53269 standard; cDNA; 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0234726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lu DAM;
                                                                                                                                                                                            05-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                  /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..463
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                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                     92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAB03627
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                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                     sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
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                                                                                                                                                                  AAA53269;
            642
                                        481
                                                                   702
                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                  Qγ
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KW antiathritic; cytostatic; antiateatic; antirheumatic; KW antiathritic; cytostatic; antiatreriosclerotic; vulnerary; Martiathritic; cytostatic; antiatreriosclerotic; vulnerary; Martiathritic; cytostatic; antiatreriosclerotic; vulnerary; Martiathritic; cytostropic; antiathritic; anti-asthmatic; vasotropic; cardiant; Mypotensive; anorectic; antiafertility; neuroleptic; anticonvulsant; Martianic; Immunosuppressive; cerebroprotective; antimicrobial; Minaulomodulator; antibacterial; antipsoriatic; thyromimetic; martiatory; antibacterial; antipsoriatic; thyromimetic; Mypotensive; antibacterial; antipsoriatic; thyromimetic; Mypotensive; antibacterial; antipsoriatic; thyromimetic; Mypotensive; antibacterial; antipsorial; dermatological; vasoconstriction; gastrointestinal disorder; cardiovascular disorder; hypertension; contextal, male infertility; impotence; testicular cancer; lung tumour; Mypotence; male infertility; impotence; testicular cancer; lung tumour; Mypotence; disease; Alzheimer; silease; Parkinson's disease; Mypotence; solisophrenia; mania; dementia; paranola; panic disorder; immunological disorder; immuno system disorder; immunological disorder; infectious disease; Mymourial lutus; immunological disorder; infectious disease; Mymourial system disorder; leavacemic brain injury; stroke; infectious disease; Mymourial system disorder; subtacemental system disorder; leavacemic product; leavacemic produ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 GGCCAACCCAAAGATGCCACGGACTGCTGCCAGACCCATGACTGCTGCTGTTGACCAC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 GGGAGGAGGGCCATCCTGCTTCGTGGCTACGGTTGCTACTGTGGGGCGGGGGGCCGT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 GGGAAAATGCCCATCCTCTTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGA 187
polycystic ovary syndrome, ectopic pregnancies, disruptions of spermatogenesis, cancers within the reproductive tract and impotence. This coding sequence was obtained from clone no.2641779, which was constructed using lung tumour tissue.
                                                                                                                                                                                                                                                                                                                                                                                                      6; Gaps
                                                                                                                                                                                                                                                                                                                                             40 GITCIGICCACAGCICACGGCAGCCIGCICAACCIGAAGGCCAIGGIGGAGGCCGICACA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 GCCCAGCCCAAGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 CTCTTTGACCAAGGCTGTCACCCCTATGTGGACCACTATGATCACACCATCGAGAACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 CAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 GACAAGAACATGGTTCTGTGCCTCATGAACCAGACGTACCGAGAGGAGTACCG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 GACAAGGAGGTGGCCTTCTGCCTGAAGCGCAACCTGGACCTACCAGAAGCG 414
                                                                                                                                                                                                                         Length 592;
                                                                                                                                                                                                            Query Match
19.5%; Score 99; DB 21; Length 59
Best Local Similarity 57.2%; Pred. No. 1.3e-15;
Matches 202; Conservative 0; Mismatches 145; Indels
                                                                                                                                                         Sequence 592 BP; 126 A; 182 C; 165 G; 119 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA encoding novel human protein NHP #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS14884 standard; cDNA; 854 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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The invention relates to novel human proteins (NHP) and the nucleic acids that encode them and antibodies raised against them.

The proteins, antibodies and nucleic acids are useful in the diagnosis, preventions and/or treatment or diseases and/or disorders are useful in the diagnosis, prognosis, prevention, asstronfestinal disorders, cardiovascular disorders (e.g. hypertension, erectile dysfunction, high blood pressure, coronary heart diseases and arteriosclerosis), anorexia, obesity, builmia, cachexia, disorders of small intestine, disorders of reproductive system, contar intertility and/or impotence), testicular cancer, lung tumours and other hyperproliferative disorders, disorders, disorders, partension's central nervous system disorders, central nervous system disorders, central nervous system disorders, immune system disorders, central nervous system disorders, immune system disorders, learning disabilities, amount, accorders (e.g. Hashimoto's thyroiditis), renal and musculo-skeletal system disorders, central nervous system disorders (e.g. multiple sclerosis, ischemic hashimoto's thyroiditis), renal and musculo-skeletal system disorders (e.g. asthma, acquired immunodeficient syndrome (AIDS), leukasemia, rheumatoid arthritis, inflammatory bovel disease, sepsis, acne, psoriasis and lupus erythematosus), neural system ceptisis, and lupus erythematosus), neural system ceptisis, respiratory disorders, olfactory disorders and NHP of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                              New human proteins, useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cardiovascular disorders, autoimmune disorders and reproductive disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 GGGAGGAGGCCCATCCTGTCCTTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGCGCTT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 GGCCAGCCCAAGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTACCAGGAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGTATGACCAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 CTCTTTGACCAAGGCTGTCACCCTATGTGGACCACTATGATCACACCATCGAGAACAAC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                          Coleman TA, Gentz RL, Endress GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 854 BP; 186 A; 254 C; 238 G; 176 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 99; DB 22;
Pred. No. 1.4e-15;
Location/Qualifiers
                                        /*tag= a
/product= "NHP #5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 294; 318pp; English.
                                                                                                                                                                                                                                                                                                                            Soppet DR,
                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 19.5%;
Best Local Similarity 57.2%;
                                                                                                                                                                                                                       03-APR-2000; 2000US-194118P.
29-SEP-2000; 2000US-236384P.
                                                                                                                                                                                 02-APR-2001; 2001WO-US10542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   2001-626394/72.
                                                                                                                                                                                                                                                                                                                          PA, Ni J,
Dillon PJ;
                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAU09096
                                                                                                   WO200174896-A1.
                                                                                                                                           11-OCT-2001
                                                                                                                                                                                                                                                                                                                              Moore PA,
Key
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40 GITCTGTCCACAGCTCACGCCAGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACA

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The present invention describes human secretory phospholipase A2 (PLA2).
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                                                         295 CAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCAGTGTGTGCCTGT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secretory phospholipase A2 (PLA2) and its encoded gene for diagnosis and treatment of secretory PLA2-associated diseases e.g. septic shock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid arthritis
   ACTGAGATAGTCTGCAGTGACCTCAACAAGACAGAGTGTGTGACAAGCAGGCATGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secretory phospholipase A2 nucleotide sequence SEQ ID NO:26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibacterial; immunosuppressive; tranquillser; vulnerary; antirheumatic; antiarthritic; septic shock; trauma; pancreatitis; allergic rhinitis; chronic rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secretory phospholipase A2; PLA2; antiallergic; antiinflammatory;
                                                                                                                                                                        407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "secretory phospholipase A2 (PLA2)"
                                                                                                                                                355 GACAAGGAGGTGGCCTTCTGCCTGAAGCGCAACCTGGACACTACCAGAAGCG
                                                                                                                  GACAAGAACATGGTTCTGTGCCTCATGAACCAGACGTACCGAGAGGAGTACCG
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                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                      AAA60878 standard; cDNA; 878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2000
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280
                                                                                                               340
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Gaps

9

19.5%; Score 99; DB 21; Length 878; llarity 57.2%; Pred. No. 1.4e-15; Conservative 0; Mismatches 145; Indels

Best Local Similarity Matches 202; Conserv

Query Match

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The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, adog, cat. horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA
                                                GGGAGGAGCGCCATCCTGCTTCGTGGGCTACGGTTGCTACTGTGGGGCTGGGGGGCCGT 159
                                                                                                                        188 GGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGTTGACCAC 247
                                                                                                                                                                                   301
                                                                                                                                                                                                                                    treatment of diseases, diagnostics, raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
                                                                                           160 GCCCAGCCCAAGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAA
                                                                                                                                                       220 CTCTTTGACCAAGGCTGTCACCCCTATGTGGACCACTATGATCACACCATCGAGAACAAC
                                                                                                                                                                                   248 CIGAAGACCCAGGGGIGCGCCATCTACAAGGACTATTACAGATACAACTT-----TTCC
                                                                                                                                                                                                                  Asundi V;
                                                                                                                                                                                                                                                                               340 GACAAGAACATGGTTCTGTGCCTCATGAACCAGACGTACCGAGAGGAGTACCG 392
                                                                                                                                                                                                                                                                                                            362 GACAAGGAGGTGGCCTTCTGCCTGAAGCGCAACCTGGACACCTACCAGAAGCG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tomato; monkey; dog; sea urchin; expressed sequence tag; ES; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human EST-derived coding sequence SEQ ID NO: 616.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 599-600; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         BP
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2000US-0617746.
2000US-0631451.
2000US-0663870.
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antibodies and research use
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03-AUG-2000;
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Whuman; cancer; ulcer; HIV infection; human immunodeficiency virus; wantiinflammatory; antirheumatic; antiarthritic; immunosuppressive; wantiinflammatory; antirheumatic; antiarthritic; immunosuppressive; wantiacterial; endocrine; cardiant; central nervous system; virucide; wanti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; we matioogical; antiallerary; antiulcer; ostoopathic; eczema; we meuroprotective; antidepressant; notropic; antidiabetic; cytostatic; meuroprotective; antidepressant; notropic; antipathis; inflammation; immunostimulant; gene therapy; antienes therapy; vaccine; inflammation; wantianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; wallergic rhinitis; diabetes; multiple sclerosis; depression; hazheiner's disease; parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                             100 GGGAGGAGCGCCATCCTGTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGCCCGT 159
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                                                                                                                                  Query Match
19.5%; Score 99; DB 22; Length 1927;
Best Local Similarity 57.2%; Pred. No. 1.8e-15;
Matches 202; Conservative 0; Mismatches 145; Indels
                                                                 Sequence 1927 BP; 413 A; 598 C; 480 G; 436 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein encoding cDNA sequence SEQ ID NO:603.
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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of the invention.
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AC AAH9
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DT 16-0
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AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
AAM25966. The proteins can have activities based on the tissues and
Calls they are expressed in, such as; antiinflammatcry; antirheumatic;
calls they are expressed in, such as; antiinflammatic;
antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
cardiovascular; antianaemic; antiagegant; haemostatic; vulnerary;
antidabetic; oxteopathic; dermatological; antiallergic; antiasthmatic;
antidabetic; cytostatic; neuroprotective; antidepressant; nootropic;
contiparkinsonian; and immunostimulaentdes are useful for screening for production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anapphylaxis, viral, bacterial, HIV and fungal infections, autolimmunity, genetic diseases, haematopoletic disorders, anaematopoletic diseases, haematopoletic disorders, anaematopoletic disorders, anaemata platelet disorders, thrombocytopaenia, wounds, burns, uncers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          osteoporosis, severe combined immunodeficienta, wounds, burns, ulcers, rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, alzheimer's disease, Parkinson's disease, neurodegenerative and neurological disorders.
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                                                                                                                       Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 GACAAGAACATGGTTCTGTGCCTCATGAACCAGACGTACCGAGAGGAGTACCG 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 19.5%; Score 99; DB 22; Length 19; Best Local Similarity 57.2%; Pred. No. 1.8e-15; Matches 202; Conservative 0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1927 BP; 413 A; 598 C; 480 G; 436 T; 0 other;
                                                                                                                                                                                               Claim 1; Page 636; 1217pp; English.
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Tang YT, Liu C, Drmanac RT;
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                                             WPI; 2001-457603/49.
                                                                          P-PSDB; AAM25827
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6; Gaps

Mismatches 145; Indels

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Conservative

Matches 202;

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WO200179446-A2
                                                     Ballinger DG,
                                        14-APR-2000:
                                           03-AUG-2000;
                                             22-SEP-2000;
           Homo sapiens.
                                          20-JUN-2000;
                        mat_peptide
                     sig_peptide
                                                        Wang D;
                                                       Liu C,
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The invention relates to polynucleotides encoding proteins CG122, CG179, CG CG55, CG121, CG162, CG27, CG153 and CG168 which are related to proteins involved in lipid metabolism and cardiovascular disease such as human equal protein sequences are useful for treating or preventing These DNA capolipoproteins, lipases and lipoprotein receptor proteins. These DNA capolipoproteins, lipases and lipoprotein receptor ALLr) cassociated with apolipoproteins, lipases and lipoprotein receptor (ALLr) cassociated with apolipoproteins, lipases and lipoprotein receptor (ALLr) cassociated with apolipoproteins, lipases and lipoprotein receptor (ALLr) captermining the presence of or predisposition to a disease associated determining the presence of or predisposition to a disease associated with altered levels of these sequences. ALLr polypeptides are also caseful for identifying a cherant expression or physiological interactions of this polypeptide. CC them and cells expressing ALLr proteins are useful for identifying a cherant expression or physiological interactions of this polypeptide. CC vectors comprising these DNA and protein sequences are also useful for the nucleic acids and polypeptides of the convention are also useful for the treatment of occlusive cardiovascular diseases, myocardial infarction, cerebral isofamental artery thrombosis cornary artery thrombosis and cerebral artery thrombosis of are used in gene therapy. The present sequence is human CG95 (or CB70)
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Ren F, Qian XB;
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lipid metabolism disorders, thrombosis and cardiovascular diseases
Human; apolipoprotein; lipase; lipoprotein receptor; ALLr; angina; cardiovascular disease; lipid metabolism; myocardial infarction; cerebral ischaemia; arterial thrombosis; thrombolytic; antilipaemic; coronary artery thrombosis; cerebral artery thrombosis; stroke; intracardiac thrombosis; gene therapy; cardiovascular; vasodilator; neuroprotectant; cerebroprotective; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Human mature CG95 (or C870) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Human CG95 (or C870) lipase protein"
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Asundi V, Zhao QA, Wehrman T, Drmanac RT,
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                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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2000US-0631451.
2000US-0667298.
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Score 99; DB 22; Length 1931; Pred. No. 1.8e-15;

19.5%; 57.2%;

Query Match Best Local Similarity

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Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillan KJ, Goddard A;
                                                                               GGCCAGCCCAAGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAA 219
                                                                                           CTCTTTGACCAAGGCTGTCACCCCTATGTGGACCACTATGATCACACCATCGAGAACAAC 279
                                                                                                                                                                           GGGAGGAGGACCATCCTGTCGTGGGCTACGGTTGCTACTGTGGGGCTGGGGGCCGT 159
                                                  40 GTTCTGTCCACAGGCTCACGGCAGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACA 99
                                                                                                                                       CTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT-----TTCC
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Kuo SS, Paoni NF,
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Klein RD,
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99WO-US05028
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Gurney AL,
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Godowski PJ,
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12-JAN-1999)
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                                                                                                                                                                                                                                                          useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by and diagnosing actious cullar, endothelial or angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The prevention, treatment and diagnosis of diseases associated with imappropriate PRO expression such as cardiovascular, endothelial or cardiac hypertrophy; For example, the nucleic acids (NCs) and vectors associated with decreased PRO expression. AAA77510 to AAA7721 and associated with decreased PRO expression. AAA77510 to AAA7721 and the present nucleotide and protein sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                                                                                                          present invention describes nucleic acids encoding PRO polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 GGGAGGAGCGCCATCCTGCTTCGTGGGCTACGGTTGCTACTGTGGGGCTGGGGGGCCGT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 GGGAAAATGCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGA 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 GITCTGTCCACAGGCTCAGGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACA 99
                                                                                                          Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or anglogenic disorders in mammals .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 18.9%; Score 95.6; DB 21; Length 496; Local Similarity 63.5%; Pred. No. 8.8e-15; hes 146; Conservative 0; Mismatches 84; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 CICITIGACCAAGGCIGICACCCTAIGIGGACCACTAIGAICACACCAI 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA sequence encoding for PRO1561 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 496 BP; 200 A; 95 C; 104 G; 95 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the exemplification of the present invention.
  Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                Claim 61; Fig 93; 315pp; English.
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                                         WPI; 2000-412154/35.
                                                                     P-PSDB; AAB24434.
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AAS21244-AAS21518 encode for novel human secretory and transmembrane
PRO polypeptides. The PRO polypeptides are useful to detect other
PRO polypeptides, to link bloactive molecules to cells expressing
PRO polypeptides, and to detect the presence of cells expressing
DRO polypeptides, and to detect the presence of mammalian lung, colon,
breast, prostate, rectal, cervical or liver tumours by comparing PRO
DOLYPEPTIDE expression in a cell sample to that in a control sample.
Come of the 275 sequences are also useful to stimulate the release of tumour necrosis factor alpha (TNF-alpha) from human blood, the
Common or differentiation of fondrocytes, the proliferation or
Common pericyte cells, the release of proteoglycans from
Commoncytes, the proliferation of inner ear utricular supporting cells or
Commoncytes, the proliferation of endothelial cells. Some of
Commoncytes, the proliferation of endothelial cells. Some of
Commoncytes, the proliferation of endothelial cells. Some of
Commoncytes, the PRO polypeptides can be used in assays to identify
Complemental muscle cells or by adipocytes; or inhibit binding of A-peptide
Complemental muscle cells or by adipocytes; or inhibit binding of A-peptide
Complemental muscle cells or by adipocytes; or inhibit binding of A-peptide
Complemental muscle cells or by adipocytes; or inhibit binding of A-peptide
Complemental muscle cells or by adipocytes; or inhibit binding of A-peptide
Complemental muscle cells or by adipocytes; or inhibit binding of A-peptide
Complemental or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gao W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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99WO-US28564
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Stewart TA, Tum
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P-PSDB; AAU12438.
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                                                                                        16-DEC-1999;
20-DEC-1999;
20-DEC-1999;
30-DEC-1999;
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18-FEB-2000;
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Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.
160 GGCCAGCCCAAGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAA 219
                                                                          18.9%; Score 95.6; DB 22; Length 496; illarity 63.5%; Pred. No. 8.8e-15; Conservative 0; Mismatches 84; Indels 0;
                                                                                                               220 CTCTTTGACCAAGGCTGTCACCCCTATGTGGACCACTATGATCACACCAT 269
                                                                                                                                  Sequence 496 BP; 200 A; 95 C; 104 G; 95 T; 2 other;
                                                                                                                                                                                                                                                                                                   DNA encoding protein of the invention #109.
                                                                                                                                                                                                                                                                                                                               Secreted; transmembrane; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 217; 787pp; English.
                                                                                                                                                                                                                      AAF54466 standard; DNA; 496 BP.
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99US-0145698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US28551.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-071395/08.
                                                                                                                                                                                                                                                                                                                                                                                         WO200078961-A1.
                                                                                                                                                                                                                                                                                                                                                              Unidentified.
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05-JAN-2000;
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30-NOV-1999;
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Gaps

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Best_Local Similarity Matches 146; Conserva

Query Match

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100 GGGAGGAGCGCCATCCTGCTTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGGCCGT 159
                                                                         160 GGCCAGCCCAAGGATGAGGTGGACTGCTGCCACGACGACTGCTGCTACCAGGAA 219
                                                                                           188 GGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCAC 247
                 Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
GITCIGICCACAGCICACGCCAGCCIGCICAACCIGAAGGCCAIGGIGGAGGCCGICACA 99
                                                                                                              220 CTCTTTGACCAAGGCTGTCACCCCTATGTGGACCACTATGATCACACCAT 269
                                                                                                                          Human PRO1561 (UNQ768) cDNA sequence SEQ ID NO:377.
                                                                                                                                                                                 AAA37132 standard; cDNA; 497 BP
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98US-0100661.
98US-0100662.
98US-0100664.
98US-0100683.
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98US-0099815.
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98US-0099642.
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98US-0100930
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02-SEP-1998;
02-SEP-1998;
02-SEP-1998;
09-SEP-1998;
09-SEP-1998;
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09-SEP-1998;
10-SEP-1998;
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15-SEP-1998;
15-SEP-1998;
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16-SEP-1998;
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98US-0101071.
98US-0101279.
98US-0101471.
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98US-0102331.
98US-0102484.
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980S-0101915.
980S-0101916.
980S-0102207.
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98US-0101475.
98US-0101476.
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9805-0105881

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9805-0106033

9805-0106178

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98US-0103711.
98US-0104257.
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98US-0105000.
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98US-0103258
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98US-0103395
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98US-0103633
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98US-0105266
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        18-SEP-1998,
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22-SEP-1998,
23-SEP-1998,
23-SEP-1998,
23-SEP-1998,
23-SEP-1998,
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24 - SEP - 1998
29 - SEP - 1998
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30-SEP-1998;
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01-OCT-1998;
01-OCT-1998;
02-OCT-1998;
06-OCT-1998;
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08-0CT-1998

08-0CT-1998

14-0CT-1998

20-0CT-1998

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30-0CT-1998
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AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences conciding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                                                                                                                                                                                                              New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 GGGAGGAGCGCCATCCTGTCGTGGGCTACGGTTGCTACTGTGGGGCTGGGGGGCCGT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCCAGCCCAAGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 GTTCTGTCCACAGCTCACGGCAGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACA 99
                                                                                                                                                                                                                                                                                Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 18.9%; Score 95.6; DB 21; Length 497; Local Similarity 63.5%; Pred. No. 8.8e-15; nes 146; Conservative 0; Mismatches 84; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 CTCTTTGACCAAGGCTGTCACCCTATGTGGACCACTATGATCACACAT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 497 BP; 201 A; 95 C; 104 G; 95 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 221; 773pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ81136 standard; cDNA; 4325 BP
                                                                                                  98US-0108867
98US-0108925
98US-0108848.
98US-0108849.
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98US-0108852.
98US-0108858.
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                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                     WPI; 2000-237871/20.
P-PSDB; AAY99450.
17 - NOV - 1998;
18 - NOV - 1998;
                                                                                                                                                                                                                   18-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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RPLA2-10; phospholipase A2; PLA2; Batten disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A human PLA2-encoding cDNA (AAQ81138) expressing HPLA2-10, was isolated from human brain RNA by RACE-FCR. 2 Rat PLA2 CDNAS, designated RPLA2-8 (AAQ81136) and RPLA2-10 (AAQ81137), were isolated from rat brain and heart CDNA libraries, respectively. A partial human genomic counterpart to RPLA2-8, HPLA2-8 (AAQ81139), was also obtained. RPLA2-8 and HPLA2-8 have been designated type III PLA2, and RPLA2-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 GCGCCATCCTGTCCTTCGTGGCTACGGTTGCTACTGTGGGCTGGGGGGCCGTGGCCAGC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAAGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAACTCTTTG 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 CCACAGCICACGGCAGCCIGCICAACCIGAAGGCCAIGGIGGAGGCCGICACAGGGAGGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            792 cerecacereageaerreregeaerrecagageargereaaacaeareagegegege 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                              Novel type III and IV low mol. wt. phospholipase A2 enzymes from humans and rats, also nucleic acid sequences useful, e.g. for recombinant prodn. of enzymes, research into Batten's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4325 BP; 1046 A; 1086 C; 1242 G; 951 T; 0 other;
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   RPLA2-8; phospholipase A2; PLA2; Batten disease; neuronal ceroid lipfuscinosis; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 57-60; 160pp; English.
                                                                            Location/Qualifiers
722..1198
/*tag= a
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                                                                                                                                                                                                                                                                              (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and HPLA2-10 as type IV.
                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-067096/09.
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                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR63044.
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                                                                                                                                                                                                                                                                                                                              Seilhamer JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease, etc.
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                                                                                                                                                                                                                                     15-JUL-1993;
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                                                      Rattus sp.
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AAO81137
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A human PLA2-encoding cDNA (AAQ81138) expressing HPLA2-10, was isolated from human brain RNA by RACE-PCR. 2 Rat PLA2 CDNAS, designated RPLA2-8 (AAQ81136) and RPLA2-10 (AAQ81137), were isolated from rat brain and heart cDNA libraries, respectively. A partial human genomic counterpart to RPLA2-8, HPLA2-8 (AAQ81139), was also obtained. RPLA2-8 and HPLA2-8 and RPLA2-9 and RPLA2-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAACTCTTTGACCAAGGCTGTCAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 GATTGGTCCTGTCGGATGCACGACGTTGTTATGGCCTACTGGAGGAGAAACACTGTGCC 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 ATGAAGCGCCTCCTCACGCTGGCTTGGTTCCTGGCTTGCAGTGTGCCTGCAGTCCCAGGG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AGCCIGCICAACCIGAAGGCCAIGGIGGAGGCCGICACAGGGAGGAGCGCCAICCIGICC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 GGCTTGCTAGAACTGAAGTCCATGATTGAGAAGGTGACTGGGAAGAATGCCGTAAAAGAAC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ITCGIGGCTACGGITGCTACTGIGGCCTGGGGGCCCTGGCCAGCCCAAGGATGAGGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGAAGAAGTICTICACCGIGGCCAICCTIGCIGGCAGCGTICTGICCACACGCICACGGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 82.8; DB 16; Length 1828;
Pred. No. 2.3e-11;
0; Mismatches 117; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel type III and IV low mol. wt. phospholipase A2 enzymes from humans and rats, also nucleic acid sequences useful, e.g. for recombinant prodn. of enzymes, research into Batten's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1828 BP; 426 A; 485 C; 489 G; 428 T; 0 other;
neuronal ceroid lipfuscinosis; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473 ATCCGGACCCAGTCCTATGACTACAGATTC 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 CCCTATGTGGACCACTATGATCACACCATC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 63-64; 160pp; English.
                                                                                                               Location/Qualifiers
233..646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.3%;
56.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seilhamer JJ, Tischfield JA;
                                                                                                                                                                                                                                                                                                                                                94WO-US07926.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 56.7
Matches 153; Conservative
                                                                                                                                                                              /*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and HPLA2-10 as type IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-067096/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease, etc.
                                                                                                                                                                                                                                                                                                                                                   15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUL-1993;
                                                                                                                                                                                                                                    W09502328-A
                                                                                                                                                                                                                                                                                             26-JAN-1995
                                                                  Rattus sp.
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Gaps

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311 CACT----ATCCAGTGCTCTGACAGGGAGGTGGTGAAAGGCAACTGTGTGGTTG 364
                                                                 339 TGACAAGAACATGGTTCTGTGCCTCATGAACCAGACGTACCGAGAGAGTACCG 392
                                                                              Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                       RESULT 15
                                                                                                                                    AAA60866
                                                                                                                                                                 g
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                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents CDNA encoding a mouse secreted phospholipase (expressed sequence tag) database, and a fragment (AAA72077) was isolated from cDNA derived from several mouse tissue types using primers AAA72078-A72081). The full length cDNA was generated using primers AAA72082-A72088 in the invention relates to the novel secreted retain phospholipase A2 activity. It also encompasses an expression retain phospholipase A2 activity. It also encompasses an expression method for the recombinant production of the protein, a method of screening potential inhibitors of the protein, a method of screening potential inhibitors of the protein, a method of a screening potential inhibitors of the protein and the compounds thus used for the diagnosis of a variety of diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
                                                                Secreted phospholipase A2; PLA2; mouse; murine; recombinant production; antibody; diagnosis; expressed sequence tag; EST; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 AGGGAGGAGGCCCATCCTGTCGTGGGCTACGGTTGCTACTGTGGGGTGGGGGGCCG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 TGGCCAGCCCAAGGATGAGGTGGACTGGTGCTGCCACGCCACGACTGCTGCTACCAGGA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 ACTCTTTGACCAAGGCTGTCACCCCTATGTGGACCACTATGATCACACCATGGAGAACAA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 CCTGAAGATGGATGCAAGAGCCTGACAGACAACTACAAATACAGGATCTCCCAGGG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 CGTTCTGTCCACAGGTCAGGCGAGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCAC 98
                                                                                                                                                                                                             /product= "Mouse mature secreted phospholipase A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 16.3%; Score 82.4; DB 21; Length 1233; Local Similarity 54.2%; Pred. No. 2.6e-11; nes 192; Conservative 0; Mismatches 156; Indels 6;
                                                                                                                                                   /product= "Mouse secreted phospholipase A2"
36..92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1233 BP; 279 A; 337 C; 307 G; 310 T; 0 other;
                                          cDNA encoding mouse secreted phospholipase A2.
                                                                                                                                                                                                                                                                                                                                                                               Mouse secretion type phospholipase A2
                                                                                                                          Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 8-10; 12pp; Japanese.
                                                                                                                                                                                                                                                                                98JP-0349602.
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                       (first entry)
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                                                                                                                                                                                                                                 JP2000166544-A.
                                                                                                   Mus musculus.
                      24-NOV-2000
                                                                                                                                                                                                                                                                                                   09-DEC-1998;
                                                                                                                                                                                                                                                                             09-DEC-1998;
                                                                                                                                                                                                                                                         20-JUN-2000.
                                                                                                                                                                   sig_peptide
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 AAA72076;
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The present invention describes human secretory phospholipase A2 (PLA2). PLA2 has antiallergic, antinflammatory, antibacterial, tranquillser, immunosuppressive, vulnerary, antirheumatic and antiarthritic activities. Human secretory phospholipase A2 (PLA2), the gene encoding it and antibodies against it are useful for the diagnosis and treatment pancreatitis, placypactated diseases e.g. septic shock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid arthritis. The present sequence encodes mouse PLA2, which is used in an example from
                                                                                                                                                                                      Mouse secretory phospholipase A2 nucleotide sequence SEQ ID NO:13.
                                                                                                                                                                                                                                                 Secretory phospholipase A2; PLA2; antiallergic; antiinflammatory;
                                                                                                                                                                                                                                                                           antibacterial; immunosuppressive; tranquillser; vulnerary; antirheumatic; antiarthritic; septic shock; trauma; pancreatitis; allergic rhinitis; chronic rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secretory phospholipase A2 (PLA2) and its encoded gene for diagnosis and treatment of secretory PLA2-associated diseases e.g. septic shock, trauma, pancreatitis, allergic rhinitis and chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= "secretory phospholipase A2 (PLA2)"
36..92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 35-36; 45pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualiflers
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             ВР
AAA60866 standard; cDNA; 1233
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                                                                                                                     02-NOV-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
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                                                                 AAA60866;
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Gaps

16.3%; Score 82.4; DB 21; Length 1233; 54.2%; Pred. No. 2.6e-11; Live 0; Mismatches 156; Indels 6;

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219 ACTCTTTGACCAAGGCTGTCACCCTATGTGGACCACTATGATCACACATCGAGAACAA 278
                                                Search completed: February 8, 2003, 04:30:03 Job time: 232 secs
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GenCore version 5.1.3

Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2003, 04:30:09; Search time 47 Seconds

(without alignments)
3308.194 Million cell updates/sec

Perfect score: 507
Sequence: 1 atgaagaagttcttcaccgt......cgccccccgccctcctag 507
Scoring table: 1 DENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Issued_Patents_NA:*

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issued_retr

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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US-08-928-361B-2	US-08-928-361B-1	US-08-440-856A-2	US-07-951-715A-2	118-08-450-4408-0	7-20** 60* 00 00	7-8585-858-80-S0	US-08-459-504B-2	118-08-459-444-2	7 11 20 00 00 00	03-03-033-349-3	US-09-547-422-2	L-912-473-511	T 011 000 001	02-03-000-120-422	US-09-160-496-4	115-08-90-080-811	T 000 000 00	US-09-307-185-1	119-08-90-080-21	2 000 000 00	US-09-307-185-3	00 500 100 100	05-750-07-60-00
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28	77.	30	31	32	33	***	#0	35	36	7.6	10	38	39		0.4	41	42	7	43	**	7	45	

ALIGNMENTS

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APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
CORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA STREET: 200 East Broward Boulevard CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IN21044-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: US 08/097,354
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                      Sequence 21, Application US/0888497; Patent No. 5972677
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: MAISO, PECET 3, 264
REGISTRATION NUMBER: 3, 264
TELECOMMUNICATION INFORMATION:
TELECHONE: 305-527-2498
TELEFAX: 305-764-4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 4325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME/KEY:
                  LOCATION:
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                                 US-09-362-230-21
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APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
APPLICANN: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Remainin Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
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                                                                                                                                                                                                                                                                                                                                                       167 CCAAGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAACTCTTTG 226
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                                                                                                                            47 CCACAGCTCACGGCAGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGA 106
                                                                                                                                                                                              107 GCGCCATCCTTCCTTCGTGGGCTACGGTTGCTACTGTGGGGCTGGGGGGCCGTGGCCAGC 166
                                                                                                                                                                                                                 Gaps
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                                                       17.4%; Score 88; DB 2; Length 4325; 60.4%; Pred. No. 2e-14; trive 0; Mismatches 95; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08/888,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21, Application US/09362230 Patent No. 6352849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
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INFORMATION FOR SEQ ID NO: 21:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                   Matches 145; Conservative
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              722..1195
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                                                                   Query Match
Best Local Similarity
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MOLECULE TYPE:
FEATURE:
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US-09-362-230-21
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US-08-888-497-21
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APPLICANT: Tischfield, Jay A. APPLICANT: Tischfield, Jay A. APPLICANT: Sellhamer, Jeffrey J. TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites NUMBER OF SEQUENCES: 44
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                                                                                                                                                                                                                                                                    167 CCAAGGATGAGGTGGACTGGTGCTGCCACGCCACGACTGCTGCTACCAGGAACTCTTTG 226
                                                                                                                                                                                                                                                                                           47 CCACAGCICACGGCAGCCIGCICAACCIGAAGGCCAIGGIGGAGGCCGICACAGGGAGGA 106
                                                                                                                                                                            107 GCGCCATCCTGTCCTTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGGCCGTGGCCAGC 166
                                                                                                                                                                                                    0; Gaps
17.4%; Score 88; DB 4; Length 4325; 60.4%; Pred. No. 2e-14; tive 0; Mismatches 95; Indels
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FILING DATE: 15-JUL-1994
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APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 21:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                      Conservative
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COUNTRY:
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APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                  47 CCACAGCTCACGGCAGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGA 106
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                                                                                                                                                                              107 GCGCCATCCTGTCCTTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGGCCGTGGCCAGC 166
                                                                                                                                                                                                                                                      167 CCAAGGATGAGGTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAACTCTTTG 226
                                                                                                                                                                                                                                                                         227 ACCAAGGCTGTCACCCCTATGTGGACCACTATGATCACACCATCGAGAACAACACTGAGA 286
                                                                                  0; Gaps
                                      17.4%; Score 88; DB 5; Length 4325; 60.4%; Pred. No. 2e-14; tive 0; Mismatches 95; Indels
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APPLICATION NUMBER: US/08/651,405
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29, Application US/08888497; Patent No. 5972677; GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1828 base pairs
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ATTORNEY/AGENT INFORMATION:
                                                                            Conservative
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REGISTRATION NUMBER: 3
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STRANDEDNESS: single
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                                                         Best Local Similarity
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PCT-US94-07926-21
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                                                                     Matches 145;
                                        Query Match
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APPLICANT: Tisoffield, Jay A.
APPLICANT: Tisoffield, Jay A.
APPLICANT: Sellhamer, Jeffrey J.
TITLE OF INVENTION: Mammallan Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
ONHESPONDENCE ADDRESS:
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                                                                                                                                         1 ATGAAGAAGTTCTTCACCGTGGCCATCCTTGCTGGCAGCGTTCTGTCCACAGGTCACGGC 60
                                                     Query Match
16.3%; Score 82.8; DB 2; Length 1828;
Best Local Similarity 56.7%; Pred. No. 3.7e-13;
Matches 153; Conservative 0; Mismatches 117; Indels 0
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REGIZERATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION:
TELEPHONE: 305-527-2498
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APPLICATION NUMBER: US 08/097,354
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Patent No. 6352849
GENERAL INFORMATION:
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APPLICATION NUMBER: 08/888,497
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INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
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LOCATION: 233..643
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               US-08-888-497-29
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LENGTH: 1828 base pairs
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APPLICANT: Tischfield, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Nucleotide
TITLE OF INVENTION: Encoded Thereby, Autisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 ATGAAGCGCCTCCTCACGCTGGCTTGGTTCCTGGCTTGCAGTGTGCCTGCAGTCCCAGGG 292
                                                                                                                                                                                                                                                                                                                                                              61 AGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGAGGAGCGCCATCCTGTCC 120
                                                                                                                                                                                                                                                                                                                                                                                     293 GGCTTGCTAGAACTGAAGTCCATGATTGAGAAGGTGACTGGGAAGAAGATGCCGTAAAGAAC 352
                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                      Similarity 56.7%; Pred. No. 3.7e-13; Similarity 56.7%; Pred. No. 3.7e-13; Conservative 0; Mismatches 117; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 CCCTATGTGGACCACTATGATCACACCATC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473 ATCCGGACCCAGTCCTATGACTACAGATTC 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US94/07926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 East Broward Boulevard
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APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US94-07926-29; Sequence 29, Application PC/TUS9407926; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
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TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Manso, Peter J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fort Lauderdale
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                       STRANDEDNESS: single
                                                                                                              NAME/KEY: CDS
LOCATION: 233..643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                     MOLECULE TYPE: CDNA
                                                linear
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US-09-362-230-29
                                                  TOPOLOGY:
                                                                                                                                                                                                                                               Matches 153;
                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                               Best Local
                                                                                            FEATURE
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APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences and Low Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TTCGTGGGCTACGGTTGCTACTGTGGGGCGGGGGGCCGTGGCCCAGCCCAAGGATGAGGTG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413 GATTGGTGCTGTCGGATGCACGTTGTTATGGGCTACTGGAGGAGAAACACTGTGCC 472
                                                                                                                                                                                                                                                                                                                  233 ATGAAGCGCCTCCTCACGCTGGCTTGCTGGCTTGCAGTGTGCTGCAGTGCTGCAGTGCTGGG 292
                                                                                                                                                                                                                                                                                       1 ATGAAGAAGTICTICACCGIGGCCAICCTIGCIGGCAGCGITCTGICCACAGCICACGGC 60
                                                                                                                                                                                                                                                ö
                                                                                                                                                                                            16.3%; Score 82.8; DB 5; Length 1828; 56.7%; Pred. No. 3.7e-13; tive 0; Mismatches 117; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473 ATCCGGACCCAGTCCTATGACTACAGATTC 502
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APPLICATION NUMBER: US/08/651,405
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FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
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US-08-888-497-31
Sequence 31, Application US/08888497
Patent No. 5972677
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                       Matches 153; Conservative
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                        233..643
                                                                     MOLECULE TYPE: CDNA
                                                                                                                                                                                                               Query Match
Best Local Similarity
                                               linear
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                                                                                                                                                                PCT-US94-07926-29
                                                                                                                    NAME/KEY:
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                                                 TOPOLOGY:
                                                                                                                                          LOCATION:
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APPLICANT: Tischfield, Jay A.
APPLICANT: Sellhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GACTGGTGCCACGCCCACGACTGCTGCTACCAGGAACTCTTTGACCAAGGCTGTCAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 57.5%; Pred. No. 1.2e-11;
Matches 138; Conservative 0; Mismatches 102; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/362,230
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FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 31, Application US/09362230
; Patent No. 6352849
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APPLICATION NUMBER: 08/888,497
                                  TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1014 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: 131..544
US-08-888-497-31
                                                                                                                                                                                           MOLECULE TYPE: CDNA
                                                                                                                                                                         linear
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                                                                                                                                                                     OPOLOGY:
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APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
OORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 ATGAAAGGCCTCCTCCCACTGGCTTGCTGCTTGTAGTGTGCCTGTGTAGGA 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGGCCGTGGCCAAGCCCAAGGATGAGGTG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.25
REFERENCE/DOCKET NUMBER: IN21044-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPENAL
SOFTWARE: PACEULA.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
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REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 200 East Broward Boulevard CITY: Fort Lauderdale
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FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
               TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
                                                                                     INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
                                                                                                                               LENGTH: 1014 base pairs
TYPE: nucleic acid
                                                                                                                                                                                         single
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                                                                                                                                                                                                                                                                                                         131..544
                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
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RESULT 11
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                                                                                                                                                                                                             15.1%; Score 76.8; DB 5; Length 1014; 57.5%; Pred. No. 1.2e-11; tive 0; Mismatches 102; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Brah, Purvi
APPLICANT: Corley, Nervi
APPLICANT: Corley, Nervi
APPLICANT: Corley, Nervi
APPLICANT: Corley, Nervi
MUMBER OF SEQUENCES: 4
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,317
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
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STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF-0403 US
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Patent No. 6103469
GENERAL INFORMATION:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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TELEPHONE: 650-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                1014 base pairs
305-764-4996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                  TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   Best Local Similarity 57.5
Matches 138; Conservative
                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                         131..544
                                                                                                                         MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3174 FOR CITY: Palo Alto
                                                                                                            linear
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                                                                                                                                                         NAME/KEY: CDS
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   TELEPHONE:
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                                                                                                              TOPOLOGY:
                                                                                                                                                                           LOCATION:
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                                                                LENGTH:
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170 AGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAACTCTTTGACC 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 TGGTTCTGTGCCTCATGAACCAGACGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCT 409
                                                                                                                                                                                                                                                             110 CCATCCTGTCCTTCGTGGGCTACGGTTGCTACTGTGGGGCGGGGGGGCCGTGGCCAGCCCA 169
                                                                                                                                                                                                                                                                                 197 CCCCCATCGCCTATATGAAATATGGTTGCTTTTGTGGCTTGGGAGGCCATGGCCAGCCCC 256
                                                                                                                                                                                                                            6; Gaps
                                                                                                                                                                                   / Match 15.0%; Score 75.8; DB 3; Length 742; Local Similarity 54.5%; Pred. No. 2.1e.11; Indels les 177; Conservative 0; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
APPLICANT: HUMAN PHOSPHOLIPASE A2 PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0403 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 ACTGCCAGGCCCCACGCCCAACTG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/966,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09489770 Patent No. 6399301 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Diskette
IBM Compatible
                  LENGTH: 742 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                  Matches 177; Conservative
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                LIBRARY: OVARTUT01
CLONE: 816403
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                                                                             linear
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                                                                                                  IMMEDIATE SOURCE:
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                                        TYPE: nucleic
STRANDEDNESS:
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                                                                                 TOPOLOGY:
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APPLICATION NUMBER: US/08/888,497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Gaps
                                                                                                                                                                                                                                           Ouery Match 15.0%; Score 75.8; DB 4; Length 742; Best Local Similarity 54.5%; Pred. No. 2.18-11; Matches 177; Conservative 0; Mismatches 142; Indels
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Fatent No. 5538885
GENERAL INFORMATION:
APPLICANT: Needham, Maurice R.C.
APPLICANT: Gooding, Clare
APPLICANT: Groding, Clare
TITLE OF INVENTION: Expression Systems
NUMBER OF SEQUENCES: 10
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FILING DATE: 27-JAN-1994
CLASSIFICATION: 435
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-885-055
TELEPAX: 650-885-0166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 742 Base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
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                                                                                                                                             linear
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                                                                                                                                                                          LIBRARY: OVART
CLONE: 816403
                                                                                                                                                           IMMEDIATE SOURCE
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                                                                                                                                           TOPOLOGY:
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APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                               REFERENCE/DOCKET NUMBER: PNK/3893/93802/MJW
TELECOMONINICATION INFORMATION:
TELEFANE: 202-861-3000
TELEFAX: 202-822-0944
TELEFAX: 671-6627 CUSH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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STREET: 200 East Broward Boulevard
APPLICATION NUMBER: US/07/810,414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/08888497 Patent No. 5972677
         ATTORNEY AGENT INFORMATION:
NAME: KOKULIS, Paul N
REGISTRATION NUMBER: 16,773
                                                                                                                                                                                                                                     LENGTH: 479 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 24..455
US-08-186-895-9
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                                                                                                                                                                                                                                                                                                             linear
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TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO:
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APPLICANT: Tischfield, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 CCACAGCTCACGGCAGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 GCGCCATCCTTCTTCGTGGGCTACGCTTGCTACTGTGGGCTTGGGGGGCCCGTGGCCAGC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 CCTCCACCCTCAGCAGCTTCTGGCAGTTCCAGAGGATGGTCAAACACATCACGGGGCGCA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.7%; Score 54; DB 2; Length 151; 61.3%; Pred. No. 8.5e-06; tive 0; Mismatches 55; Indels
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STREET: 200 East Broward Boulevard
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SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
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                                                        APPLICATION NUMBER: US/08/651,405
                                                                                                APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08/888,497
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Patent No. 6352849
GENERAL INFORMATION:
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IBM PC compatible
                                                                                                                                                                       NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: INZ
                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
                                                                                                                                                                                                                                                                                                                                                      LENGTH: 151 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                    TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 61.3
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 200 East Browe CITY: Fort Lauderdale
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                CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-888-497-26
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FILING DATE
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APPLICANT: Tischield, Jay A. APPLICANT: Seilhamer, Jeffrey J. APPLICANT: Seilhamer, Jeffrey J. APPLICANT: Seilhamer, Seilhamer J. APPLICANT: Seilhamer J. APPLICANT: Sequences and Low Molecular Weight Amino Acid Sequences TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 CCACAGCTCACGGCAGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGA 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 200 East Broward Boulevard CITY: Fort Lauderdale
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APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-UUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                       IN21044-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26, Application PC/TUS9407926
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 CCAAGGATGAGGTGGACTGGTG 188
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                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
                                              NAME: Manso, Peter J. REGISTRATION NUMBER: 32,264
                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 26:
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FILING DATE: 26-JUL-1993 ATTORNEY/AGENT INFORMATION:
                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 151 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                     305-764-4996
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                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
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Best Local Similarity
                                                                                                                                                                                                                                                                                           linear
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us-09-975-456b-1.rni

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 base pairs
; TVPE: nucleic acid
; TYPE: nucleic acid
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA

Query Match

Query
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Sequence 63, Appl
Sequence 597, Appl
Sequence 70, Appl
Sequence 216, Appl
Sequence 125, Appl
Sequence 622, Appl
Sequence 42, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 14, Appl
Sequence 3, Appli
Sequence 1495, Appli
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                                                                                                                                                                                                                       February 8, 2003, 05:15:59 ; Search time 55 Seconds
    (without alignments)
    4369.446 Million cell updates/sec
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'Cgn2_6'(ptodata/2/pubpna/USO7_puBCOMB.seq:*
'Cgn2_6'(ptodata/2/pubpna/USO6_puBCOMB.seq:*
'Cgn2_6'(ptodata/2/pubpna/USO6_puBCOMB.seq:*
'Cgn2_6'(ptodata/2/pubpna/USO6_puBCOMB.seq:*
'Cgn2_6'(ptodata/2/pubpna/USO8_puBCOMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-121-049-533
US-10-121-049-533
US-10-124-591-2
US-10-144-591-2
US-09-965-832-63
US-09-925-300-70
US-09-925-300-70
US-09-924-456-125
US-09-924-456-125
US-09-925-297-52
US-09-925-297-52
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US-09-476-242-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_NA:*
                                                                                                                                              OM nucleic - nucleic search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Match Length DB ID
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Maximum DB seq length: 200000000
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Sequence 66, Appl
Sequence 340, App
Sequence 340, App
Sequence 343, App
Sequence 345, App
Sequence 18, Appl
Sequence 18, Appl
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TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PT055p1
CURRENT APPLICATION NUMBER: US/09/969,384
CURRENT PILING DATE: 2001-10-03
PRIOR PPLICATION NUMBER: PCT/US01/10542
PRIOR FILING DATE: 2001-04-02
PRIOR PILING DATE: 2001-04-02
PRIOR PLILING DATE: 2000-09-29-9
PRIOR PLILING DATE: 2000-09-29-9
PRIOR PLILING DATE: 2000-09-29-9
PRIOR FILING DATE: 2000-09-29-9
PRIOR FILING DATE: 2000-04-03
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5, Appl
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          Sequence 6, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCTTTGACCAAGGCTGTCACCCCTATGTGGACCACTATGATCACACCATCGAGAACAAC 279
                                                                                                                                                                       Sequence 26, Sequence 26, Sequence 16, Sequence 17, Sequence 11, Sequence 11, Sequence 19, Sequence 10, Sequence 11, Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 GTTCTGTCCACAGGTTCACGGCAGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACA 99
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19.5%; Score 99; DB 9; Length 854;
Best Local Similarity 57.2%; Pred. No. 4.3e-18;
Matches 202; Conservative 0; Mismatches 145; Indels
                                               US-09-216-393-340

US-09-216-393-342

US-09-216-393-343

US-09-216-393-345

US-09-476-242-19

US-09-476-242-20

US-09-476-242-20

US-09-476-242-20

US-09-476-242-20

US-09-476-242-10

US-09-476-242-15

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US-09-476-242-12
                     US-09-905-370-2
US-09-989-920-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09969384 Publication No. US20020192749A1 GENERAL INFORMATION:
     NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-384-6
   US-09-969-384-6
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CURRENT APPLICATION NUMBER: US/10/028,072 CURRENT FILING DATE: 2001-12-19
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NR APPLICATION NUMBER: 60/062816

NR FILING DATE: 1997-10-24

NR APPLICATION NUMBER: 60/063045

NR FILING DATE: 1997-10-24

NR APPLICATION NUMBER: 60/063082

NR APPLICATION NUMBER: 60/063082

NR FILING DATE: 1997-10-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT AFPLICATION WORDLAND COURRENT PLLING DATE: 2001-12-19 PRIOR PILING DATE: 1997-06-18 PRIOR FILING DATE: 1997-06-18 PRIOR PLICATION NUMBER: 60/056974 PRIOR PLICATION NUMBER: 60/056974 PRIOR PLICATION NUMBER: 60/059113 PRIOR FILING DATE: 1997-09-17 PRIOR PLICATION NUMBER: 60/059115 PRIOR FILING DATE: 1997-09-17 PRIOR PILING DATE: 1997-09-17 PRIOR PLILING DATE: 1997-09-17 PRIOR APPLICATION NUMBER: 60/059117 PRIOR PLILING DATE: 1997-09-17 PRIOR APPLICATION NUMBER: 60/059117 PRIOR APPLICATION NUMBER: 60/059117
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R APPLICATION NUMBER: 60/059588
R FILING DATE: 1997-09-19
R PLILING DATE: 1997-09-18
R FILING DATE: 1997-09-24
R APPLICATION NUMBER: 60/062250
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FILING DATE: 1997-10-17
FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/062287
FILING DATE: 1997-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; sequence 533, Application US/10028072; Publication No. US20030004311A1; GENERAL INFORMATION:
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APPLICATION NUMBER: 60/059263
FILING DATE: 1997-09-18
APPLICATION NUMBER: 60/059352
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APPLICATION NUMBER: 60/059184
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Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
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Filvaroff, Ellen
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FILE REFERENCE:
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                                                                       241 CTGAAGACCCAGGGGTGCAGCATCTACAAGGACTATTACAGATACAACTT-----TTCC 294
                                                                                                                                           340 GACAAGAACAIGGIICIGIGCCICAIGAACCAGACGIACCGAGAGGAGIACCG 392
                                                                                                                                                                                                                                                                    155 GACAAGGAGGTGGCCTTCTGCCTGAAGCGCAACCTGGACACCTACCAGAAGG 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09835996A Patent No. US20020142953A1
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Montgomery, Julie
Tang, Y. Tom
Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
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Wehrman, Tom
Drmanac, Radoje
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Matches 202; Conservative
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Qian, Xiahong
Wang, Dunrui
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US-09-835-996A-5
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237 CIGAAGACCCAGGGGIGCGGCAICIACAAGGACIATTACAGAIACAACIT-----TICC 290
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PRIOR APPLICATION NUMBER: 60/063127
PRIOR FILING DATE: 1997-10-27
PRIOR FILING DATE: 1997-10-28
PRIOR PLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-28
PRIOR PLICATION NUMBER: 60/063561
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PRIOR PLICATION NUMBER: 60/063704
PRIOR PLICATION NUMBER: 60/063734
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PRIOR PLICATION NUMBER: 60/07323
PRIOR PLICATION NUMBER: 60/07333
PRIOR PLICATION

PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1998-04-15
PRIOR PILING DATE: 1998-04-24
PRIOR PILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-13
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PRIOR PELICATION NUMBER: 60/085339
PRIOR PILING DATE: 1998-05-13
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PRIOR PELING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-12
PRIOR PELING DATE: 1998-05-12
PRIOR PELING DATE: 1998-05-12
PRIOR PELING DATE: 1998-05-12
PRIOR PELING DATE: 1998-05-10
PRIOR PELING DATE: 1998-05-10 FILING DATE: 19/98-06-11 APPLICATION NUMBER: 60/089532 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089599
FILING DATE: 1988-06-17
APPLICATION NUMBER: 60/089907 APPLICATION NUMBER: 60/089947 PRIOR APPLICATION NUMBER: 60/090445 PRIOR FILING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/090538 PRIOR FILING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/091519 PRIOR FILING DATE: 1998-07-02 PRIOR APPLICATION NUMBER: 60/091982 PRIOR FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/090863 APPLICATION NUMBER: 60/091360 FILING DATE: 1998-06-19 FILING DATE: 1998-06-18 PRIOR FILING DATE: 1998-06-24 FILING DATE: 1998-06-26 1998-06-2 FILING DATE: 1998-07-0 PRIOR PRIOR PRIOR PRIOR

Query Match
18.9%; Score 95.6; DB 9; Length 496;
Best Local Similarity 63.5%; Pred. No. 3e-17;
Matches 146; Conservative 0; Mismatches 84; Indels 0; Gaps

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APPLICANT:
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                                                                                                                         160 GGCCAGCCCAAGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAA 219
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                                                                                                                                             100 GGGAGGAGCGCCATCCTGTCGTGGGCTACGGTTGCTACTGTGGGGCTGGGGGCCGT 159
                                                                        18.9%; Score 95.6; DB 9; Length 496; 63.5%; Pred. No. 3e-17;
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0; Mismatches 8
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Publication No. US20030022239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-121-049-533
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Gerritsen, Mary E.
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Wood, William
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Desnoyers,Luc
Filvaroff,Ellen
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Matches 146; Conservative
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APPLICANT:
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160 GGCCAGCCCAAGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAA 219
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RACE: P3330RACE: P3330RACE
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
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Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
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                                                                                               ; Sequence 533, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
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DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
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Wood, William
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DeForge, Laura
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Gurney, Austin L.
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Filvaroff, Ellen
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                                                                 RESULT 5
US-10-123-904-533
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC160
CURRENT APPLICATION NUMBER: US/10/140,470
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
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63.5%; Pred. No. 3e-17;
Live 0; Mismatches 84; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10124591
Patent No. US2002017720841
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
Gao, Wei-Olang
Gerrisen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
M. E.
                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION; 396
; OTHER INFORMATION: unknown base
US-10-140-470-533
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Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                Watanabe,Colin K
Wood,William
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 146; Conservative
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                                                                                                                   Tumas, Daniel
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                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo Sapien
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                             496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
US-10-124-591-2
                                                                                                APPLICANT:
                           APPLICANT:
                                                        APPLICANT:
                                                                                   APPLICANT:
                                                                                                                                             APPLICANT:
                                                                                                                APPLICANT
                                                                                                                                APPLICANT
                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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Sequence 63, Application US/09962832

Patent No. US20020110821A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
CURRENT PELICATION NUMBER: US/09/962,832
CURRENT APPLICATION NUMBER: US/00/235,077
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 AGGATCAGGTGGACTGGTGCTGCCACGCCACGACTGCTACCAGGAACTCTTTGACC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 AAGGCTGTCACCCCTATGTGGACCACTATGATCACACCATCGAGAACAACACCTGAGATAG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 TCCTGTGCGGACCGGCAGAGAATCCCAAGAACTGTTGTGCAAGTGTGAGGAGA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    431 TIGCTAACTGCTTAGCCCAAACTGAGTACAACTTAAAGTACCTCTTCTACCCCCAGTTCC 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 TGGTTCTGTGCTCATGAACCAGACGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.0%; Score 75.8; DB 9; Length 742; 54.5%; Pred. No. 1e-11; tive 0; Mismatches 142; Indels
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                             APPLICATION NUMBER: US/09/489,770
FILING DATE: <unknown>
APPLICATION NUMBER: 08/966,317
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,591
FILING DATE: 16-Apr-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                      TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 742 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         491 TATGTGAGCGGACTCGCCCAAGTG 515
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                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: OVARTUT01
CLONE: 816403
                                                                                                                                                                                                                                                                                                                                                                  COPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 54.59
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-962-832-63/c
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121 TTCGTGGGCTACGGTTGCTACTGTGGGGGCGGCCGTGGCCAGCCCAAGGATGAGGTG 180
                                                                                               181 GACTGGTGCCACGCCCACGACTGCTGCTACCAGGAACTCTTTGACCAAGGCTGTCAC 240
                                                                                                                                                           196 ATGAAGACCCTCCTACTGTTGGCAGTGATCATGATCTTTGGCCTACTGCAGGCCCATGGG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGAGGAGCGCCATCCTGTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TTCGTGGCTACGGTTGCTACTGTGGGGGGGCCGTGGCCAGGCCGAAGGATGAGGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GACTGGTGCTGCCACGACTGCTGCTACCAGGAACTCTTTGACCAAGGCTGTCAC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.4%; Score 57.8; DB 10; Length 1076; 52.2%; Pred. No. 1.1e-06; Live 0; Mismatches 117; Indels 0;
                                                                                                                                                                                                                                                                                                     Sequence 70, Application US/09925300

Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
TITLE OF INTENTION: Nucleic Acids, Proteins and Antibodies
TITLE OF INTENTION: Nucleic Acids, Proteins and Antibodies
CURRENT APPLICATION NUMBER: US/09/925,300
FILE REPERENCE: PAIO1
CURRENT FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
MINNER OF SEA IN NACE 1000
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 52.28
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature LOCATION: (911)
                                                                                                                                                                                                                               376 ACCAA 380
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TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE REFERENCE: 689200-70
CURRENT APPLICATION NUMBER: US/09/969,708
PRIOR APPLICATION NUMBER: US/60/237,606
PRIOR PAPLICATION NUMBER: US/60/237,608
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR SEC ID NOS: 658
SOFTWARE: Patentin Version 3.0
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                                                                                                                                                                                                                                                                                          230 AAGGCTGTCACCCCTATGTGGACCACTATGATCACACCATCGAGAACAACACTGAGATAG 289
                                                                                                                                                                                                      7; Gaps
                                                                                                                                                                                                                                                                                                                                                              273 GAGGAGGCCGCTGCAGGCCCCAAGACGCGCTACTCCTGGCAGTGCGTCAATCAGAGCG 214
                                                                                                                                                                                                                                                                                                                                                                                            350 TGGTICTGTGCCTCATGAACCAGACGTACCGAGAGGAGTACCGTGGCTTCCTCAATGTCT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 ATGAAGACCCTCCTACTGTTGGCAGTGATCATGATCTTTGGCCTACTGCAGGCCCATGGG 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGAAGAAGTTCTTCACCGTGGCCATCCTTGCTGGCAGCGTTCTGTCCACAGCTCACGGC 60
                                                                                                                                                         13.0%; Score 65.8; DB 10; Length 445; 52.6%; Pred. No. 4.8e-09; tive 0; Mismatches 147; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.4%; Score 57.8; DB 10; Length 854;
52.2%; Pred. No. 9.8e-07;
tive 0; Mismatches 117; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 ACTGCCAGGCCCCACGCCCAACTG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 597, Application US/09969708
Patent No. US20020102532A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
)
OTHER INFORMATION: n=a,t,g or c
US-09-962-832-63
SOFTWARE: Patentin version 3.0 SEQ ID NO 63
                                                                                                                                                                                Matches 171; Conservative
                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 128; Conservative
                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homosapiens
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Best Local Similarity
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                                                                                                                                                     Query Match
                                                                             FEATURE
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TITLE OF INVENTION: Sets

FILE REPERENCE: 689290-76

CURRENT APPLICATION NUMBER: US/09/954,456

CURRENT FILING DATE: 2001-09-18

PRIOR PELICATION NUMBER: US/60/234,052

PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR APPLICATION NUMBER: US/60/234,923

PRIOR FILING DATE: 2000-09-25

PRIOR PELING DATE: 2000-09-25

PRIOR PLICATION NUMBER: US/60/235,134

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-26

PRIOR PELING DATE: 2000-09-26

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 67.8%; Pred. No. 1.2e-06;
Matches 80; Conservative 0; Mismatches 38; Indels 0
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                     PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1225, Application US/09954456; Patent No. US20020115057A1; GENERAL INFORMATION:
                                                                                                                                                                    NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patentin version 3.0
SEQ ID NO 822
LENGTH: 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin version 3.0
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Best Local Similarity 67.8%
Matches 80; Conservative
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                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Young, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-954-456-1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-954-456-1225
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SEQ ID NO 1225
LENGTH: 562
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                           TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
TITLE OF INVENTION: Sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc CURRENT PRINCES 689290-76

GURRENT APPLICATION NUMBER: US/69/234,456

CURRENT APPLICATION NUMBER: US/60/233,617

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-25

PRIOR PRIOR APPLICATION NUMBER: US/60/235,134

PRIOR PRIOR APPLICATION NUMBER: US/60/235,37
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1 Similarity 67.8%; Pred. No. 1.2e-06;
80; Conservative 0; Mismatches 38;
                                                                                              FILE KEREMENEL: BUSJUD-16
CURRENT PAPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR PELING DATE: 2001-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
PRIOR PELING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR PELING DATE: 2000-09-25
PRIOR PELING DATE: 2000-09-25
PRIOR PELING DATE: 2000-09-25
PRIOR PELING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
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PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
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APPLICATION NUMBER: US/60/235,720
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FILING DATE: 2000-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 822, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 2276
                                                                                     FILE REFERENCE: 689290-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo saplens
US-09-954-456-216
APPLICANT: Young, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER: Paten
SOFTWARE: Paten
SEQ ID NO 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-954-456-822
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APPLICANT: Phippard, Deborah
APPLICANT: Vasanthakamur, Geetha
APPLICANT: Vasanthakamur, Geetha
APPLICANT: Ma, Xiao-Jun
TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides,
TITLE OF INVENTION: vectors, and cells
CURRENT APPLICATION NUMBER: US/09/765,231A
NUMBER OF SEQ ID NOS: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
155 GCCGTGGCCAGCCCAAGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTGGTA 212
                 201 GCTCAGGCACCCCCGTGGATGAACTGGACAAGTGCTGCCAGACACATGACAACTGCTA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 TCACAGGGAGGAGCGCCATCCTGTCGTGGGCTACGGTTGCTACTGTGGGGTGGGGG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 GCCGTGGCCAGCCCAAGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTGGTA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
CURRENT APPLICATION NUMBER: US/09/225,297
CURRENT APPLICATION NUMBER: US/09/225,297
CURRENT APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.3%; Score 57.2; DB 10; Length 630; 67.8%; Pred. No. 1.3e-06; ative 0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: 1-854
; LOCATION: unknown
; OTHER INFORMATION: unsure at all n locations
US-09-765-231A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (556)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEF: misc feature
LOCATION: (628)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                     Sequence 52, Application US/09925297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42, Application US/09765231A Patent No. US20020119452A1 GENERAL INFORMATION.
APPLICANT: Searle/Monsanto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 67.89
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                 RESULT 14
US-09-925-297-52
                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 52
LENGTH: 630
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US-09-765-231A-42
                                                                                                                                                                                                                                                                                                                                                                                                 DNA
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LENGTH: 854
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149 ATGAAGACCCTCCTACTGTTGGCAGTGATCATGATCTTTGGCCTACTGCAGGCCCATGGG 208
                                                                                                   61 AGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGAGGGCGCCATCCTGTCC 120
                                                                                                                    0; Gaps
                                                  1 ATGAAGAAGTTCTTCACCGTGGCCATCCTTGGTGGCAGCGTTCTGTCCACAGCTCACGGC 60
                                                                                                                                                  121 TTCGTGGGCTACGGTTCCTACTGTGGGCCTGGGGGCCCGTGGCCCAAGGATGAGGTG 180
                                                                                                                                                                  Length 854;
Ouery Match
Best Local Similarity 53.5%; Pred. No. 5.8e-06;
Matches 115; Conservative 0; Mismatches 100; Indels
                                                                                                                                                                                                     181 GACTGGTGCTGCCACGCCCACGACTGCTGCTACCA 215
                                                                                                                                                                                                                   Search completed: February 8, 2003, 06:43:54
Job time : 58 secs
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February 8, 2003, 02:43:59; Search time 1939 Seconds (without alignments) 4234.715 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                               16154066 seqs, 8097743376 residues
                                                                 OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                      Scoring table: IDENTITY_NUC Gapoxt 1.0
                                                                                                                                                                                  US-09-975-456B-1
                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                     Run on:
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32308132 Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

gb_htc:* gb_est3:* gb_est4:* gb_est5:* em_estfun:* em_gss_hum:* em_esthum:*
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gb_estl:* em_gss_inv:* em_gss_pln:* em_estba:* gb_est2:* dp_gss:* EST: * Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_other:* em_gss_pro:*

em_gss_rod:*

em_gss_vrt:* em_gss_fun:* em_gss_mus:*

em_gss_mam: *

A1173803 ue92c03.y A1931322 u167f12.y A1574411 uk20911.y A1173890 ue92h04.y AW106043 um22d03.y BB613865 BB613865 Description SUMMARIES 657 10 BB613865 511 9 A1173803 486 9 A1931322 484 9 A1574411 452 9 A1173890 455 10 AWIO6043 Query Match Length DB ID 50.4 36.8 33.1 32.6 28.8 Score 255.4 186.4 167.8 165.2 146 138 . 0 Result

TCBAP10 um55d06 510989 6021058 6030847 97101 M BS32003	A143041 VV49h02.y BBB69347 BB869347 BE138146 ug49a11.y AK018005 Mus muscu AA/62051 Vv49h02.r B0570398 g1149e02. AK004232 Mus muscu AK060516 AL660516 BQ418599 11x5sa07.y	BE015249 127486 MAAW292929 UI-H-BWO-BW087924 011-H-BWO-BW087924 011-H-BWO-BW087924 012-H-BWO-BW087920 011-H-BWO-BW0887020 011-H-BW0-BW088700 011-H-BW0-BW08870 011-H-BW0-BW08870 011-H-BW0-BW08870 011-H-BW0-BW08870 011-H-BW0-BW0-BW08870 011-H-BW0-BW0-BW0-BW0-BW0-BW0-BW0-BW0-BW0-BW0	DE00095 BR00095 N93958 2274 [64.51 BB61576 BR1576 BC964576 602812255 BM926265 AGBNCOURT BE12874 DEPA5524 AV691515 AV691515 AV695229 AV695522 AV698272 AV698272
BM153087 AW213414 BM106914 BF781906 B1836812 AW659630 BM363855 BF077514	BB869347 BE138146 AK018005 AA762051 BQ570398 AK004232 AL660516 BQ418599	BE015249 BM087924 BM087924 BM087924 BM593389 BM565033 AI769633 BM688463 BM688506 BM688506 BM18115 BF150826 BB866695	N93958 BB615766 BC964576 BM9264576 BE128774 AV691515 AV695929
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4 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	367 472 1582 501 446 1206 620 620	0 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	445 587 834 1590 381 396 398
19.6 19.6 18.7 18.3 17.6 17.6 17.4 16.4	10 10 10 10 10 10 10 10	1 1 1 1 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3	m ni ni ni ni ni ni ni
	1998.8	75.8 75.8 75.8 73.6 73.6 70.2 70.2 70.2 68.2	655 .8 655 .8 665 .4 664 .8 664 .2 667 .2
7 8 8 10 11 12 13 14 15	16 118 12 22 23 23	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	C 38 39 44 44 45 45

ALIGNMENTS

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RIKEN integrated sequence analysis (RISA) system--384-format RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi,Y., Shibata,K., Itch,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa,Y., F., Fukuda,S., Hara,M., Itch,M., Kawai,J., Shibata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, 172-186 (2001 genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci,P., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
Prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,M., Ohara,E.,
wagi,K., Fujiwake,S., Inoue,K., Togawa,M., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Site1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ITCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGGCCGTGGCCAGCCCAAGGATGAGGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGAGCGCCATCCTGTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 AGCCTGCTGAAGCTGAAGTCCATGGTGGAGGCCATCACACAGAAAACTCCATCCTGTCC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 ATGAAGAAATTCTTTGCCATCGCAGTCTGGCCGGCAGTGTGTAACCACGGCCCACAGC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RIKEN full-length enriched, 0 day neonate head"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGAAGAAGTICTICACCGIGGCCAICCTIGCIGGCAGCGIICTGICCACAGGICACGGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="head"
/dev_stage="0 day neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="4831444E21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 298; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e mouse tissues.
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/note—weetor: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
/note=avector: pME18S-FL3; Site_1: brail cDNA was primed
Site_2: DraIII (CACCATGTG); lst strand cDNA was primed
with an oligo(dT) primer [ATGTGGCTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
cloth. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | (bases 1 to 511)
| Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
| Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
| Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
| Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 07-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ue92c03.yl Sugano mouse embryo mewa Mus musculus cDNA clone
IMAGE:1498564 5' sinilar to SW:PA24_RAT P39878 14 KD PHOSPHOLIPASE
A2 PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                  181 GACTGGTGCTGCCACGCCCACGACTGCTACCAGGAACTCTTTGACCAAGGCTGTCAC 240
                                                                                                                                                       241 CCCIATGIGGACCACTAIGAICACACCAICGAGAACAACACIGAGAIAGICIGCAGIGAC 300
                                                                                                                                                                               359 TITGIGGCTACGGCTGCTACTGCGGGCTGGGGGGACGCGGCCATCCCATGGATGAGGTA 418
                                                                          301 CTCAACAAGACAGGGGGGGAAGCAGGCATGCATGTGTGAGAACAAGAACATGGTTCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      waterson, N.
The WashU-HMMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL"
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/dev stage="embryo, 14 dpc"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: custom primer used
High quality sequence stop: 442.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               511 bp
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Fax: 314 286 1810
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IMAGE:2135663 5' similar to SW:PA2C_HUMAN P39877 CALCIUM-DEPENDENT
PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (basa: Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Bonderwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter Kohn, S., Shin, T., Pape, D., Harvey, N., Schurk, R., Ritter Waterston, R. and Wilson, R.
                                                                                                                                                                                           251 ATGAAGAATTCTTTGCCATGGCAGTCCTGGCCGGCAGTGTGGTAACCACGGCCCACAGG 310
                                                                                                                                                                                                                               61 AGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGAGGGCGCCATCCTGTCC 120
                                                                                                                                                                                                                                                  121 TTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGCCCGTGGCCAGCCCAAGGATGAGGTG 180
                                                                                                                                                                                                                                                                                                                        181 GACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAACTCTTTGACCAAGGCTGTCAC 240
                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
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                                                                                                 Length 511;
                                                                                       Score 186.4; DB 9; Length Pred. No. 3.3e-36; 0; Mismatches 46; Indels
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CTTCTGCTCTAAAAGCTGCG and 3' end primer
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/clone_lib="Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
                 CGACCTGCAGCTCGAGCACA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 CCCTATGTGGACCACTATGA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   491 CCCTACGTGGACCACTATGA 510
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                                                                                       Query Match
Best Local Similarity 82.3%;
Matches 214; Conservative
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AI931322
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double-stranded cDNA was ligated to a Draill adaptor [TGTTGGCTACTGG], digested and cloned into distinct Draill stress of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). Mold be used to isolate the cDNA insert. Size selection was performed to exclude fragments cl.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CGACCTCGAGAGAGA."
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IMAGE:1969604 5' similar to SW:PA2C_HUMAN P39877 CALCIUM-DEPENDENT
PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.
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Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter Waterston, R., and Wilson, R.

The Mashlowin Mouse EST Project 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGAAGAAGTTCTTCACCGTGGCCATCCTTGGTGGCAGCGTTCTGTCCACAGGTCACGGC 60
                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M.Washu-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fel: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.1%; Score 167.8; DB 9; Length 486; 81.8%; Pred. No. 1.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                  43; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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/organism="Mus musculus"
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                        /strain="C57BL"
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Best Local Similarity 82.7%;
Matches 167; Conservative (
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                      137 C
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AW106043
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                                        1 (bases 1 to 452)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Galsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 07-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ue92h04.yl Sugano mouse embryo mewa Mus musculus cDNA clone
IMAGE:1496615 5' similar to SW:PA24_RAT P39878 14 KD PHOSPHOLIPASE
A2 PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                   121 TTCGTGGGCTACGGTTGCTACTGTGGGGGGGGGCCGTGGCCAGCCCAAGGATGAGGTG 180
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                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                  DB 9; Length 484;
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                                                                                                                                                                                                                                                                                                                              43; Indels
    /clone_lib="Sugano mouse embryo mewa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                                                                                                                                                                32.6%; Score 165.2; DB 9
81.6%; Pred. No. 6.2e-31;
tive 0; Mismatches 43
                   /dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
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SOURCE
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AI173890
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/ tow_nost__times.
//note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
//note="Vector: pmer | farged conditions |
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ArgGGCTTATTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCTACTGG], digested and cloned into distinct DraIII
Sites of the pME18S-FL3 vector ($' site CACTGTGTG', 3' site
CACCATGTG, Xhoi should be used to isolate the cDNA
cACCATGTG, Xhoi should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTGTGGCTGCAGCTGGAGCACA."

CGACCTGCAGCTGGACCACA."

On the part of the primer of the primer capacity of the primer of the primer of the primer capacity of the primer of the primer of the primer capacity of the primer of the primer of the primer capacity of the primer of the primer
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Marra,M., Hiller,L., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
Underwood,K., Steptoe,M., Pape,D., Harvey,N., Schurk,R., Pitter
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Materston,R. and Wilson,R.
Unpublished (1999)
Contact: Marra M,Washlo-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park, Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ő
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 455)
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IMAGE:2225285 5' similar to TR:042187 042187 PHOSPHOLIPASE A2 ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGAGCGCCCATCCTGTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGAAGAAGTICTICACCGIGGCCAICCTIGGIGGCAGCGITCTGICCACAGCICACGGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 3.8e-26;
0; Mismatches 35; Indels
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                                                                                                      /clone_lib="Sugano mouse embryo mewa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 t
                                                                                                                                            /dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455 bp
/db_xref="taxon:10090"
/clone="IMAGE:1498615"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 g
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//doce="Vector: lambda pSB; Site_l: BamHI; Site_2: ECORI;
First strand cDNA was primed with an anchored
XhOT-oligo(dT) primer [5'GGAGACTCGAGCGCGCAGGAGGAG(T)VN
3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand
was primed with a BamHI-dC primer
[5'AGAGACTCGGATCGCGCCCCAATAATAATAATAAT(C) 3']
Double-stranded cDNA was then digested with BamHI and XhOI
and directionally cloned into the BamHI and SalI sites of
lambda pSB vector. Library went through one round of
normalization. Library was constructed by Wei Yu at RIKEN
of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
Itoh M, Nagaoka S, Sasakin, Okazaki Y, Muramatau M,
Schneider C, Hayashizaki Y, High efficiency selection of
full-length cDNA by improved biotinylated cap trapper.,
DNA Res 4: 1, 61-6, Feb 28, 1997)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                     /clone_lib-"Pediatric pre-B cell acute lymphoblastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 TICTGTCCACAGCTCACGGCAGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 GGAGGAGCGCCATCCTGCTTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGGCGGTG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 GCCAGCCCAAGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAAC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 TCTTTGACCAAGGCTGTCACCCCTATGTGGACCACTATGATCACACCATCGAGAACAACA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 TGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT-----TTCCC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW213414 51 51 5 mRNA 11 near EST 15-M um55d06.yl Sugano mouse embryo mewa Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 19.6%; Score 99.6; DB 13; Length 463; Best Local Similarity 57.4%; Pred. No. 1.4e-14; Matches 202; Conservative 0; Mismatches 144; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1111 | 1 | 1 | 1 | 1 | 1 | 1 | 394 ACAAGGAGGTGGCCTTCTGCCTGAAGGCGAACCTACCAGAAGGG 445
                                                                                                                                                                                                                                                leukemia Baylor-HGSC project-TCBA"
/sex="male"
                                                                                                                                                                                                                                                                                                                  /cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
                                                                                                                                                                                                                                                                                                /tissue_type="leukopheresis"
                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                      Location/Qualiflers
                                                                                                                                                                                                 /clone="TCBAP1356"
                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
                                                       Email: clones@txccc.org
                                                                           Seq primer: M13 primer
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                                Fax: 832-825-4038
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                                                                                                                                                                                                                                                                                                             /note="Vector: DME185-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGCCCTTTTTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor!
[TGTTGGCTACTGG], digested and cloned into distinct DraIII
sites of the pME185-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). Xhol should be used to isolate the cDNA
linsert. Size selection was performed to exclude fragments
(University of Tokyo Institute of Medical Science).
CTGGCTGACTGAAAGGCTGG and 3' end primer
CTGGCTGACAGCAGG and 3' end primer
CGACCTGCACGACGGCAG.

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Wel, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman, F.R. Jr., Gunaratne, P.H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F. Pediatric Leukemia cDNA Sequencing Project (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine 1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM153087

463 bp mRNA linear EST 30-NOV-20 TCBAF1013560 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens CDNA clone TCBAP1356, mRNA
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 ATGAAGAAATTCTTTGCCATCGCAGTCCTGGCCGGCAGTGTGGTAACCACGGCCCACAGC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGAGGAGCGCCATCCTGTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TTCCTGGGCTACGTTGCTACTGTGGGGCTGGGGGGCCGTGGCCAGGCCAAGGATGAGGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGAAGAAGTICTICACCGTGGCCATCCTTGCTGGCAGCGTTCTGTCCACAGCTCACGGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

27.2%; Score 138; DB 10; Length 455;
Best Local Similarity 82.5%; Pred. No. 3.7e-24;
Matches 170; Conservative 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Indels
                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="IMAGE:2225285"
/clone_lib="Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL"
                                          Seq primer: custom primer used
High quality sequence stop: 440.
Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GACTGGTGCTGCCACGCCCACGACTG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430 GACTGGTGCTGCCATGCCCACGACTG 455
                                                                                                                                                                                                                                                                                           /lab_host-"DH10B
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                           MGI:1005481
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6; Gaps

EST 15-MAR-2000

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950 DP mRNA linear EST 12-JAN-2001 602105856F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4234596 5', mRNA sequence.
  l (bases 1 to 484)
Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T.,
Casas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S. C., Bennett,
G. L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A., Chitko-McKown, C. G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                         Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
                                                                                                                                                  Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 CAGGGGAAAGTCCCAGTGTTCCACCAAGGGAAGTGGTGAGCAGCAGCAGCTGTGCGCCTGT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 GGCCAGCCCAAGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 CTCTTTGACCAAGGCTGTCACCCTATGTGGACCACTATGATCACACCATCGAGAACAAC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 CIGAAATCTGACAACTGTGACATCGACCACTATGACTACACCTT----TTTC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 GGGAGGAGCGCCATCCIGTCCTTCGTGGCTACGGTTGCTACTGTGGGGTTGGGGGCGCCGT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 GGGAAGATCCCCATCTTCTTCTTTCACACTATGGCTGTTACTGCAGAAAAGGTGGCCAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 GITCTGTCCACAGGTCACGGCAGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.7%; Score 94.6; DB 13; Length 484; 58.2%; Pred. No. 2.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                USDA, ARS, US Meat Animal Research Center Po Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plate: 104 row: K column: 22 seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and -minmatch 12 options.
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 188; Conservative
                                                                                                                                                                                                                                                                   Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGG, 3' site
CACCATGTG), xhoI should be used to isolate the CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insert. Size selection was performed to exclude fragments (1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CITCIGCICIAAAAGCIGCG and 3' end primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
  Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 533)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,E., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGAGGAGCGCCA-TCCTGTC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 ATGAAGAAATTCTTGCCATGCGCAGTCCTGGCCGCAGTGTGGTAACCACGGCCCACAGC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGAAGAAGTICITCACCGIGGCCAICCTIGCIGGCAGCGTICTGICCACAGCICACGGC 60
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                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTICGIGGGCIACGGIIGCIACIGIGGCIGGG-GGGCCGIGGCCAGCCCAAGGAI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
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510989 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
BM106914
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                                                                                                                                                                                                                                      Contact: Marra M/washU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib-"Sugano mouse embryo mewa"
/dev.stage="embryo, 14 dpc"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: custom primer used
High quality sequence stop: 465.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGACCTGCAGCTCGAGCACA."
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/clone="IMAGE:2259179"
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                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                      Unpublished (1999)
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REFERENCE AUTHORS Matches 141;

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Query Match

BASE COUNT

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RESULT 9 BM106914 ACCESSION KEYWORDS

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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMGGE:4234566"
/clone="IMGE:4234566"
/clone="lb="NoT_CGAP_K1014"
/lab_host="DH10B" (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCWV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NoT_CGAP Library. |"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI886812 680 bp mRNA linear EST 04-0CT-2001 603084703F1 NIH_MGC_120 Homo saplens cDNA clone IMAGE:5223912 5',
                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                      1 (bases 1 to 950)
NIH WGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 CCACAGCTCACGGCAGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 CCTCCACCTCAGCAGTTTCTGGCAGTTCCAGAGGATGGTCAAACACGTCACAGGGCGCA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 GCGCCATCCTCCTTCGTGGGCTACGGTTGCTACTGTGGGGCTGGGGGCCGTGGCCAGC 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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18.3%; Score 93; DB 12; Length 950;
Best Local Similarity 57.5%; Pred. No. 8.3e-13;
Matches 187; Conservative 0; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                   Plate: LLAM9839 row: o column: 13
High quality sequence stop: 583.
                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref-"taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain-"FVB/N"
                  BF781906.1 GI:12086942
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at:
http://image.linl.gov. e column: 01
                                                                                                1 (bases 1 to 680)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MCC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 TCACGGCAGCCTGCTCAACCTGAAGGCCATGGTGGAGGCCGTCACAGGGAGGAGGAGCCCAT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 CCTGTCCTTCGTGGGCTACGGTTGCTACTGTGGGCGGGGGGGCCGTGGCCAGGCCAAGGA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 TCCAGGGGGATCCTGAACCTGAACAGATGGTCAAGCAAGTGACTGGGAAAATGCCCAT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 GTGCAGCATCTACAAGACTATACAGATACAACTT-----TTCCCAGGGGAACATCCA 302
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High quality sequence start: 4
High quality sequence stop: 680.
Location/Qualifiers
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/clone_lib="NIH_MGC_120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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331 TGCATGTGTGACAAGA 346
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JOURNAL
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                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                         1 (bases 1 to 392)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Waray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Lagareid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                             EST 25-APR-2001
                                                                                                                                                                                                       Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                       Sequence evaluation of four pooled-tissue normalized bovine cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 GAGAACAACACTGGAGATAGTCTGCAGTGACCTCAACAAGACAGAGTGTGACAAGCAGACA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 GCCGTCACAGGGAGGAGGCGCCATCCTGTCCTTCGTGGGCTACGGTTGCTACTGTGGGCTG 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 GCTTCCAGTGGTGTGGGTCCAGCCGAGGTGACATACTGGACCTGAACGAGATGGTCAGA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 CAAGTGACGGGAAGATCCCCATCTTCTTCTATTCACACTATGGCTGTTACTGCAGAAAA 199
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                                                                                                                                                                                                                                                                                                                                                                                            libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 21180013
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                                               AW659630 392 bp mRNA linear 97101 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
Fax: 402 762 4390
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0; Mismatches
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Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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/clone_lib="MARC 1BOV"
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/lab_host="DH10B"
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AW659630.1 GI:7425457
                                                                                                                                                                                                                  Mammalia; Eutheria;
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Tel: 217 333 5998

Fax: 217 244 5617

Email: h-lewin@uiuc.edu

Funding for Cattle EST sequencing was provided by the USDA National

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Funding for Cattle EST sequencing was provided by the USDA National

Fasearch Initiative, Project No. 98-35205-6644, and a grant from

the Japanese Ministry of Agriculture Fisheries and Forestry to

H.A.Lewin and J.E. Momack. Base-Calling/Quality scores: PHRED form

Mashington University Genome Center. Vector trimming: Cross_Match

from Washington University Genome Center PHRAP suite. This sequence

is vector free and at least 200bp in length.

Insert Length: 558 Std Error: 0.00

Plate: BS320033000 row: E column: 8

Seq primmer: CCCAAGCTGAAATTAACCC

Bight Active Column: Repairs Active Column: Rep
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                                                                                                                                                                                                                              EST 10-JAN-2002
                                                                                                                                                                                                                                                              BS320033000E8 Subtracted Lewin Cattle Spleen Bos taurus CDNA clone BS320033000E8 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2002)
Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 558)
Lewin, H.A., Soares, M.B., Pardinas, J., Liu, L. and Larson, J.H.
Subtracted Lewin Cattle Spleen ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 89.2; DB 13; Length 558; Pred. No. 6.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9913"
/clone="BS320033000E8"
/clone_lib="Subtracted Lewin Cattle Spleen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123; Indels
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Location/Qualifiers
                                                                                                                                                                                                                                              558 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Angus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM363855.1 GI:18107224
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58.1%;
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374 TGCGCCTGTGACAAGA 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus
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1 (bases 1 to 495)
Smith T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fehrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                EST 25-APR-2001
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, and encal, and encometrium."
182 TGTGACATCAGCTTCGACCACTATGACTACCTT----TTTCCAGGGGAAAGTCCAG 235
                                                                                                                                                             TGTCACCCCTATGTGGACCACTATGATCACCCATCGAGAACAACACTGAGATAGTCTGC 294
                                                                                                                                                                                     165 GCCCTCCCTTGCTCTACGTGAAATACGGCTGCTTTTGTGGTCTGGGGGGCCATGGCCAGC 224
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                                                                                                                                                                                                                                                                                                                                                                                                                    BF077514 495 bp mRNA linear 227437 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
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PO Box 166, Clay Center, NE 68933-0166, USA
TED: 402 762 4366
Fax: 402 762 4369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACKWARD: GTTTTCCCAGTCACGACG
Plate: 88 row: D column: 20
Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH108"
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Best Local Similarity 56.7%
Matches 186; Conservative
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                                                                                                                                                                                                                                                                                                    296 TTCTGCCT 303
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BF077514
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MEDLINE
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' arranded with a Not I - oligo(dT) primer [5' arranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
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Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A143024)
Av49h02.y1 Soares_thymus_thyms_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thymys_thym
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
167 CCAAGGATGAGGTGGACTGGTGCTGCCACGCCACGACTGCTGCTACCAGGAACTCTTTG 226
                                                                                                                                                                                                                                                                                                                                                              347 ACATGGTTCTGTGCCTCATGAACCAGACGTACCGAGAGTACCGTGGCTTCCTCAATG 406
                                                    339 GTGTCAAGTGTGAACCAACGGAGACAAATGCCAAGAACTCATATGCAAGTGTGACCAGG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 AGTITGCTCACTGCTTAGCCCGAGCAGAGTACAACATTAAGTACCTCTTCTATCCCCATT 458
                                                                                                                                                                             227 ACCAAGGCTGTCACCCCTATGTGGACCACTATGATCACACCATGGAGAACAACACTGAGA
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/clone_11b="Soares_thymus_2NbMT"
/sex="male"
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/db_xref="taxon:10090"
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/lab_host="DH108"
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                                                                                                                                                                                                 99 AGGGAGGAGCGCCATCCTTCTTCGTGGGCTACGGTTGCTACTGTGGGCTGGGGGGCCG 158
                                                                                                        159 TGGCCAGCCCAAGGATGAGGTGGACTGGTGCTGCCACGCCCACGACTGCTGCTACCAGGA 218
                                                                                                                                                  123 AGGGCAACCCAAAGATGCCACAGACTGGTGGTGTGATGATGTTGCCCA 182
                         6; Gaps
                                            39 CGTICTGTCCACAGGCTCACGGCAGCCTGCTCAACCTGAAGGCCCATGGTGGAGGCCGTCAC 98
                                                          Ouery Match
Best Local Similarity 54.2%; Pred. No. 2e-10;
Matches 192; Conservative 0; Mismatches 156; Indels
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Search completed: February 8, 2003, 05:46:24 Job time : 1947 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein . protein search, using sw model

February 10, 2003, 10:35:27; Search time 36 Seconds Run on:

(without alignments) 621.836 Million cell updates/sec

US-09-975-456B-2 957

Perfect score: Sequence:

1 MKKFFTVAILAGSVLSTAHG........EPPPEEVTCSHQSPAPPAPP 168

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1985.DAT:*
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| SIDS2/gcgdata/geneseq/geneseqp_embl/AA2001_DAT:*
| SIDS2/gcgdata/geneseq/geneseqp_embl/AA2001_DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* A_Geneseq_101002:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human lipid metabo Novel human protei Human secretory ph Human prospholipas Human CG95 (or C87 Human EST encoded Human protein segu Mouse secreted pho Mouse secretory ph Mouse secretory ph
ΩI	ABB08202 AAU09096 AAB03627 AAB03627 AAE11924 AAB11994 AAB12536 AAB12810
DB	23 22 22 22 22 21 21 21
Length	211 145 145 1445 1444 1424
Query e Match Length DB I	1000 36.9 36.9 36.8 36.8 36.0 36.0 32.8
Score	957 352 352 352 352 354 354 313 513 513 513 513 513 513 513 513 513
Result No.	100843351

phosp syncy syncy syncy syncy phosps prosts prosts prosts prosts rype x-type x-type group group group pross	BOVING PLAZ protei
AABB1021 AABB1022 AAPB3363 AAPB3363 AAPB3112 AAR25416 AAR63055 AAR63053 AAR6308154 AAM08154 AAM49005 AAR63046 AAR63046 AAR63046 AAR63046 AAR63046 AAR63046 AAR63046 AAR63046 AAR63046 AAR63046 AAR63044 AAR63044 AAR63044 AAR63044 AAR63044 AAR63044 AAR63044 AAR63044 AAR63044 AAR63044 AAR63044 AAR63044	1
22 100 100 100 100 100 100 100 100 100 1	
1442 1444 1444 1444 1444 145 145 146 146 146 146 146 146 146 146 146 146	
22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	
313.5 30.5 30.5 30.5 30.5 30.5 30.5 30.5 3	
11111111111222222222211111111111111111	

ALIGNMENTS

Human lipid metabolism enzyme-2 (LME-2). ABB08202 standard; Protein; 211 AA. 04-MAR-2002 (first entry) ABB08202; RESULT 1 ABB08202

Human; LME-2; lipid metabolism enzyme-2; cytostatic; neuroprotective; immunosuppressive; anti-inflammatory; cardiovascular; gene therapy; enzyme therapy; cancer; neurological disorder; autoimmune disorder; inflammatory disorder; cardiovascular disorder.

SEG 20 NOIZ of the publicabu 11-MAY-2001; 2001WO-US15210. WO200185956-A2. Homo sapiens. 15-NOV-2001.

25-MAY-2000; 2000US-207903P. 07-JUN-2000; 2000US-210150P. 23-JUN-2000; 2000US-213392P. 11-MAY-2000; 2000US-203511P

Talle H

(INCY-) INCYTE GENOMICS INC.

Das D, Reddy R, Yao MG, Nguyen DB, Lu Y, Tribouley CM, Yue H; Khan FA, Gandhi AR, Au-young J, Lal P, Kearney L, Elliott vS; Ding L, Thornton M;

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The sequence represents a novel human lipid metabolism enzyme (LME-2) of
the invention. The invention relates to novel human LME's, and the
comply the invention relates to novel human LME's, and the
polynucleotides which identify and encode them. The enzymes of the
invention have cytostatic, neuroprotective, immunosuppressive,
comit inflammatory, and cardiovascular activity. The polypeptides and
polynucleotides have a use in gene therapy and enzyme therapy. The lipid
compouls enzymes are useful in the diagnosis, treatment and prevention
compounds menzymed isorders, autoimmune/inflammatory disorders, and
cordiovascular disorders, and in the assessment of the effects of
cardiovascular disorders, and in the assessment of the effects of
cardiovascular disorders, and in the assessment of the effects of
compounds on the expression of nucleic acid and amino acid
compounds that modulate the activity of LME. Polynucleotides encoding
compounds that modulate the activity of LME. Polynucleotides encoding
compounds that modulate the activity of energe to detect and
compounds in the disease, to generate a transcript image of a
tissue or cell type, to generate hybridization probes useful in mapping
the naturally occurring genomic sequence, and for screening libraries of
compounds in drug screening techniques. The polypeptide sequences may be
used to analyse the proteome of a tissue or cell type. Oligonucleotide
primers derived from polynucleotide sequences encoding LME may be used to
cetect single nucleotide polymorphisms.
                                                                                      New lipid metabolism enzymes useful for diagnosing, treating and preventing cancer, neurological disorders, autoimmune/inflammatory disorders, and cardiovascular disorders
                                                                                                                                                                                                                          Claim 1; Page 109; 122pp; English.
                        2002-089794/12.
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Length 211; Indels Query Match 100.0%; Score 957; DB 23; Best Local Similarity 100.0%; Pred. No. 3.7e-81; Matches 168; Conservative 0; Mismatches 0; Sequence 211 AA;

44 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 103 1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60 g

DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120 104 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNWYLC 163 ò g

121 LMNQTYREEYRGFLNVYCQGPTPNCSIYEPPPEEVTCSHQSPAPPAPP 168 ŏ g

AAU09096 standard; Protein; 145 AA. AAU09096; RESULT 2 AAU09096

Novel human protein NHP #5. 20-DEC-2001 (first entry)

Human; novel human protein; NHP; antidiabetic; antirheumatic; antiarthritic; cytostatic; antiarteriosclerotic; vulnerary; neuroprotective; notropic; antiparkinsonian; vasotropic; cardiant; anti-human immunodeficiency virus; antiasthmatic; vasotropic; cardiant; hypotensive; anorectic; antiinfertility; neuroleptic; anticonvulsant; antimanic; immunosuppressive; cerebroprotective; antimicrobial; antiinflammatory; antibacterial; antipsoriatic; thyromimetic; immunomodulator; antiseborrheic; dermatological; vasoconstriction; gastrointestinal disorder; cardiovascular disorder; hypertension; cachexia; male infertility; impotence; testicular cancer; lung tumour; hyperproliferative disorder; pulmonary system disorder;

central nervous system disorder; bone disorder;
neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
Huntington's disease; Schizophrenia; mania; dementia; paranoia;
panic disorder; learning disability; amyotropic lateral sclerosis;
psychosis; autism; sleep disorder; immune system disorder;
Hashimoto's thyroiditis; musculo-skeletal system disorders;
multiple sclerosis; ischaemic brain injury; stroke; infectious disease;
adabetes mellitus; immunological disorder; asthma; AIDS; immunogen;
acquired immunodeficient syndrome; leukaemia; rheumatoid arthritis;
inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus;
neural system disorder; respiratory disorder; olfactory disorder; wound healing.

Homo sapiens.

52..65 /label= Immunogenic_epitope /label= Immunogenic_epitope 37..105 Immunogenic_epitope /label= Immunogenic_epitope /label= Immunogenic_epitope Location/Qualifiers 11...129 /label= Imr 136. Region Region Region Region Region

WO200174896-A1.

11-OCT-2001.

02-APR-2001; 2001WO-US10542.

29-SEP-2000; 2000US-236384P. 03-APR-2000; 2000US-194118P.

(HUMA-) HUMAN GENOME SCI INC

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0; Gaps

Soppet DR, Coleman TA, Gentz RL, Endress GA; Moore PA, Ni J, Li Y, Dillon PJ;

WPI; 2001-626394/72. N-PSDB; AAS14884.

New human proteins, useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cardiovascular disorders, autoimmune disorders and reproductive disorders

Claim 11; Page 306-307; 318pp; English.

The invention relates to novel human proteins (NHP) and the concision and the nucleic acids that encode them and antibodies raised against them. In the proteins, antibodies and nucleic acids are useful in the diagnosis, The proteins, antibodies and nucleic acids are useful in the diagnosis, prevention and/or treatment or diseases and/or disorders convolution vasoconstriction, erectile dysfunction, high blood pressure, cachexia, disorders of small intestine, disorders of reproductive system cachexia, disorders of small intestine, disorders of pulmonary system, and other hyperproliferative disorders, disorders of pulmonary system, and other hyperproliferative disorders, bone disorders, neurodegenerative contral nervous system disorders, bone disorders, disorders disease, Parkinson's disease, Huntington's disease, schizophrenia, mania, dementia, paranola, consider, learning disabilities, amyotropic lateral sclerosis, psychoses, autism, sleep disorders (e.g. multiple sclerosis, ischemmic contral nervous system disorders (e.g. multiple sclerosis, ischemmic contral injury and/or stroke), infectious diseases, diabetes mellitus, immunological disorders (e.g. asthma, acquired immunodeficient syndrome contral sequence represents an NHP of the invention.

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                                                                                                                                                       63 CCHAHDCCYQELFDQGCHPYVDHYDRTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM 122
                                                                                                                                                                            63 CCQTHDCCYDHLKTQGCSIYKDYYRYRFSQG-NIHCSD-KGSWCEQQLCACDKEVAFCLK 120
                                                                      Gaps
                                                                                        7 VAILAGSVLSTA----HGSLLNLKAMVEAVTGRSAILSFVGYGGYCGLGGRGQPKDEVDW 62
                                                                                                                    3 LALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secretory phospholipase A2; PLA2; antiallergic; antinflammatory; antibacterial; immunosuppressive; tranquillser; vulnerary; antirheumatic; antiarthritic; septic shock; trauma; pancreatitis; allergic rhinitis; chronic rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secretory phospholipase A2 (PLA2) and its encoded gene for diagnosis and treatment of secretory PLA2-associated diseases e.g. septic shock, trauma, pancreatitis, allergic rhinitis and chronic
                                                                      œ
                                                                                                                                                                                                                                                                                                                                                                                                                        Human secretory phospholipase A2 protein sequence SEQ ID NO:27.
                                     Length 145;
                                                                   52; Indels
                            ch 36.9%; Score 353; DB 22; I Similarity 45.5%; Pred. No. 3.7e-25; 66; Conservative 19; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                      121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
                                                                                                                                                                                                                                                                                                                          AAB12537 standard; Protein; 145 AA.
                                                                                                                                                                                                                    123 N--OTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ishizaki J, Suzuki N, Hanasaki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 41; 45pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..10
/label= signal
21..145
/label= PLA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-JP06844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98JP-0349608
                                                                                                                                                                                                                                                                                                                                                                                         02-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SHIO ) SHIONOGI & CO LTD.
                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-423429/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rheumatoid arthritis
 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA60878.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-DEC-1998;
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   Sednence
                                                                                                                                                                                                                                                                                                                                                             AAB12537;
                                Query Match
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                                                            Matches
                                                                                                                                                                                                                                                                                                             AAB1253
                                                                                                                                                                                                                                                                                                RESULT
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63 CCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 CCQTHDCCYDHLKTQGCGIYKDYYRYNFSQG-NIHCSD-KGSWCEQQLCACDKEVAFCLK 120
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                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                     7 VAILAGSVLSTA----HGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDW 62
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                                                                                                        Length 145;
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                                                                                                                                                                                     52; Indels
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                                                                                      36.8%; Score 352; DB 21;
45.5%; Pred. No. 4.6e-25;
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/label- putative_mature_HPPL1
                                                                                                                      45.5%; Pred. ...
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                                                                             Query Match
Best Local Similarity 45.58
Matches 66; Conservative
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    145 AA;
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Sequence
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                                                                                                      The present sequence is human phospholipase I (HPPLI). This protein is involved in the hydrolysis of membrane phospholipids. The protein and its coding sequence can be used to diagnose and treat the following: cancers such as prostate, breast and testicular cancers, autoimmune and inflammatory disorders such as AIDS, allergies, anaemia, asthma, atheroselerosis, Crohn's disease, diabetees mellitus, emphysema, Graves' disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, psoriasis, rheumatoid arthritis and systemic lupus erythematosus, infection caused by viruses, fungi, bacteria, parasites and protozoa, and reproductive disorders including infertility, disruptions of the menstrual cycle, polycystic overy syndrome, ectopic pregnancies, disruptions of spermatogenesis, cancers within the reproductive tract
                                                                                                                                                                                                                                                                                                                                                                                                                            63 CCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM 122
                                                                                                                                                                                                                                                                                                                                                                                                                                           63 CCQTHDCCXDHLKTQGCGIYKDYXRYNFSQG-NIHCSD-KGSWCEQQLCACDKEVAFCLK 120
                                     Human phospholipase genes and proteins useful to diagnose, prevent or treat cancer, autoimmune or inflammatory or reproductive disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; apolipoprotein; lipase; lipoprotein receptor; ALLr; angina; cardiovascular disease; lipid metabolism; myocardial infarction; cerebral ischaemia; arterial thrombosis; thrombolytic; antilipaemic; coronary artery thrombosis; cerebral artery thrombosis; stroke; intracardiac thrombosis; gene therapy; cardiovascular; vasodilator; neuroprotectant; cerebroprotective.
                                                                                                                                                                                                                                                                                                                                                                         7 VAILAGSVLSTA----HGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDW 62
                                                                                                                                                                                                                                                                                                                                                                                             8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human mature CG95 (or C870) protein"
                                                                                                                                                                                                                                                                                                                       36.8%; Score 352; DB 21; Length 145; 45.5%; Pred. No. 4.6e-25; Live 19; Mismatches 52; Indels
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25..145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human CG95 (or C870) lipase protein.
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                                                                                  Claim 1; Page 70-71; 80pp; English.
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                                                                                                                                                                                                                                                                                                                                                      66; Conservative
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       2000-350750/30
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Best Local Similarity
                                                                                                                                                                                                                                                                                                   145 AA;
                     N-PSDB; AAA53269
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                                                                                                                                                                                                                                                                                                     Sequence
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The invention relates to polynucleotides encoding proteins CG122, CG179, CG654, CG121, CG162, CG27, CG153 and CG168 which are related to proteins involved in lipid metabolism and cardiovascular disease such as human polipoproteins. lipases and lipoprotein receptor proteins. These DNA apolipoproteins and lipoprotein receptor proteins. These DNA can protein sequences are useful for treating or preventing disorders expression and for treating lipid metabolism, cardiovascular diseases and thrombosis. Antibodies against these proteins are useful for and thrombosis. Antibodies against these proteins are useful for cardiovascular diseases and thrombosis. Antibodies against these proteins are useful for useful for identifying agents (agonists and antagonists) that bind to therm and cells expressing ALLr proteins are useful for identifying a cherant expression or physiological interactions of this polypeptide. Overtors comprising these DNA and protein sequences are also useful for use in treatment of occlusive cardiovascular diseases, myocardial infarction, cerebral isothemia, angina, arterial chrombosis, coronary artery thrombosis and cerebral artery thrombosis of the invention are also useful for the reatment of occlusive cardiovascular chrombosis, coronary artery thrombosis and cerebral artery thrombosis of are used in gene therapy. The present sequence is human CG95 (or C870)
                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding human apolipoproteins, lipases, and lipoprotein receptor polypeptides, useful for preventing diagnosing and treating lipid metabolism disorders, thrombosis and cardiovascular diseases
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                                                                                                                                                                                                                           Goodrich R;
                                                                                                                                                                                                                                                            Qian XB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8;
                                                                                                                                                                                                                                 Tang TY, Zhou P, Goc
Drmanac RT, Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.8%; Score 352; DB 22; 45.5%; Pred. No. 4.6e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human EST encoded protein SEQ ID NO: 1625.
                                                                                                                                                                                                                                    Montgomery JR,
QA, Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM24100 standard; Protein; 145 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 N--QTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Fig 1; 266pp; English.
                        2000US-0598042.
2000US-0631451.
2000US-0667298.
                                                                                                                                                                                                                                                                Asundi V, Zhao QA,
   2000US-197137P
                                                                                                               17-NOV-2000; 2000US-0714936
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                                                                                                                                                                                                                                          Loeb D,
                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-611724/70.
N-PSDB; AAD19218.
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nes 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 AA;
                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lipase protein.
                                                                                                                                                                                                                                       Ballinger DG,
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14-APR-2000;
                                                       03-AUG-2000;
22-SEP-2000;
                                 20-JUN-2000;
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                                                                                                                                                                                                                                                                                                  Wang D;
                                                                                                                                                                                                                                                                            ပဲ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 CCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polypeptide for treatment of diseases, diagnostics, raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
antibacterial; endocrine; cardiant; central nervous system; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 VAILAGSVLSTA----HGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDW 62
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3 LALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW 62
                Human; sheep; plg; cow; fruit fly; yeast; hamster; macaque; horse;
tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
diagnostics; forensic test; gene mapping; genetic disorder;
blodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                                           Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
A, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.8%; Score 352; DB 22; Length 145; 45.5%; Pred. No. 4.6e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match
Local Similarity 45.5%; Pred. NO. *...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 1102; 1275pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 RNLDIYQKRLRFYWRPHCRGQIPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM25827 standard; Protein; 150 AA.
                                                                                                                                                                                   25-JAN-2001; 2001WO-US02687.
                                                                                                                                                                                                                                17-JUL-2000; 2000US-0617746. 03-AUG-2000; 2000US-0631451.
                                                                                                                                                                                                                25-JAN-2000; 2000US-0491404.
                                                                                                                                                                                                                                                               15-SEP-2000; 2000US-0663870
                                                                                                                                                                                                                                                                                                                                                                                                                                    antibodies and research use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (flrst entry)
                                                                                                                                                                                                                                                                                                                                         Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-476164/51
                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 AA;
                                                                                                                                                                                                                                                                                                                            Liu C,
                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAH98759,
                                                                                                                       WO200154477-A2.
                                                                                            Homo sapiens,
                                                                                                                                                      02-AUG-2001.
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AAM25966 to AAH99904 encode the human proteins given in AAM25255 to
CC AAM25963. The proteins can have activities based on the tisques and
cells they are expressed in, such as: antiniflammatory; antirheumatic;
antiarthritic: immunosuppressive; antibacterial; endocrine: cardiant;
cardiavascular; antianaemic; antiagregant; heemostatic; unimaragen;
cardiavascular; antianaemic; antiagregant; heemostatic; unimaragen;
cardiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
antiparkinsonian; and immunostimulant. The proteins and polynucleotides
concoding them can be used in gene therapy, antisense therapy and vaccine
concoding them can be used in gene therapy, antisense therapy and vaccine
concoding them can be used in gene therapy, antisense therapy and vaccine
concoding them can be used in gene therapy, antisense therapy and vaccine
concoding them can be used in gene therapy, antisense therapy and vaccine
concoding them can be used in gene tivity of a protein e.g. inflammation,
concorpostulosy, cardiac anaphytaxis, viral, bacterial, HIV and fungal
infections, autoimmunity, genetic diseases, hematopoietic disorders,
costeoporosis, asthma, diabetes, cancer, multiple sclerosis, depression,
contentions, asthma, diabetes, cancer, multiple sclerosis, depression,
contentions and disorders.
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                          antiaggragant; haemostatic; vulnerary; antiulcer; osteopathic; eczemn; dermatological; antiallergic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antialergic; antissthmatic; antiparkinsonian; infection; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; antianaphylactic; rheumatoid antibatic; septic shock; pancreatitis; autoimmunity; genetic disease; haematopoletic disorder; plateled disorder; asthma; thrombocytopaenia; osteoporasis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; alreiner's disease; parkinson's disease; neurodegenerative disorder;
anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 CCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :1:1 | 1: | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:1 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 278; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT, Liu C, Drmanac RT;
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                                                             neurological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200153455-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2001.
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a mouse secreted phospholipase A2 (secreted PLA2). A cDNA was initially identified in an EST (expressed sequence tag) database, and a fragment (AAA72077) was isolated from cDNA derived from several mouse tissue types using primers AAA72078-A72081). The full length cDNA was generated using primers AAA7208-A72088. The invention relates to the novel secreted PLA2, nucleic acids encoding it, and variants of the protein which retain phospholipase A2 activity. It also encompasses an expression vector and host cells comprising DNA encoding murine secreted PLA2, a method for the recombinant production of the protein, a method of screening potential inhibitors of the protein and the compounds thus identified, and an antibody specific for murine PLA2. The antibody can be used for the diagnosis of a variety of diseases.
                                                                                                                                                                                                                                      Secreted phospholipase A2; PLA2; mouse; murine; recombinant production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 CHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLMN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 CQKHDCCYAHLKIDGCKSLTDNYKYSISQGT-IQCSD-NGSWCERQLCACDKEVALCLKQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 VAILAGSVL---STAHGSLLNLKAMVEAVIGRSAILSFVGYGCYCGLGGRGQPKDEVDWC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                       antibody; diagnosis; drug screening; expressed sequence tag; EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 36.0%; Score 344.5; DB 21; Length 144; Local Similarity 45.1%; Pred. No. 2.3e-24; ns 65; Conservative 20; Mismatches 52; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                    "Mouse mature secreted phospholipase A2"
                                                                                                                                                                                                                                                                                                                                         /note= "Signal peptide"
20. 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse secretion type phospholipase A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 10-11; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 -- QTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NLDSYNKRLRYYWRPRCKGKTPAC 144
                 126 RNLDTYQKRLRFYWRPHCRGQTPGC 150
                                                                                                             AAB11994 standard; Protein; 144 AA
123 N--QTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                              Mouse secreted phospholipase A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98JP-0349602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98JP-0349602
                                                                                                                                                                               24-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-458171/40.
N-PSDB; AAA72076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            JP2000166544-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-DEC-1998;
                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                              AAB11994;
                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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The present invention describes human secretory phospholipase A2 (PLA2). PLA2 has antiallergic, antiinflammatory, antibacterial, tranquillser, immunosuppressive, vulnerary, antirheumatic and antiarthritic activities. Human secretory phospholipase A2 (PLA2), the gene encoding it and antibodies against it are useful for the diagnosis and treatment of secretory PLA2-associated diseases e.g. septic shock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid arthritis. The present sequence represents mouse PLA2, which is used in an example from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 CHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLMN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 VAILAGSVL---STAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secretory phospholipase A2 (PLA2) and its encoded gene for diagnosis and treatment of secretory PLA2-associated diseases e.g. septic shock, trauma, pancreatitis, allergic rhinitis and chronic
                                                                                                                                                                                                    Secretory phospholipase A2; PLA2; antiallergic; antiinflammatory; antibacterial; immunosuppressive; tranquillser; vulnerary; antirheumatic; antiarthritic; septic shock; trauma; pancreatitis; allergic rhinitis; chronic rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length 144;
                                                                                                                                                      Mouse secretory phospholipase A2 protein sequence SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.0%; Score 344.5; DB 21; Length 45.1%; Pred. No. 2.3e-24; tive 20; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 37; 45pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanasaki K;
AAB12536 standard; Protein; 144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- QTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20..144
/label= PLA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-JP06844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98JP-0349608.
                                                                                                         02-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ishizaki J, Suzuki N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-423429/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAA60866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200034486-A1.
                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
                                                           AAB12536;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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This invention relates to human secretory phospholipase A2 (PLA2) protein and the gene encoding it. Inhibitors of phospholipase A2 have antibacterial; immunosuppressive; antinitammatory; tranquilliser; vulnerary; antiasthmatic; antiallergic; antirheumatic; and antiarthritic activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in the diagnosis of PLA2 associated diseases e.g. septic shock, adult respiratory distress syndrome, pancreatitis, trauma, bronchial asthma, allergic rhinitis and rheumatoid arthritis. The present sequence is used in the invention for the identification and characterisation of the human PLA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secretory phospholipase A2 and encoded gene, useful in diagnosis of and screening drug candidates for treating associated diseases e.g. septic shock, adult respiratory distress syndrome and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.8%; Score 313.5; DB 22; Length 142; 42.2%; Pred. No. 1.7e-21; tive 20; Mismatches 58; Indels 7;
                           adult respiratory distress syndrome; ARDS; bronchial asthma; allergic rhinitis; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                /note- "Mature phospholipase A2"
                                                                                                                                                                                                                          /label- Signal_peptide
                                                                                                                                                                                                                                                         20..142
/label- Mature_PLA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 LMN--QTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ishizaki J, Suzuki N, Hanasaki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 42; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB81022 standard; Protein; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-SEP-2000; 2000WO-JP06344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99JP-0266616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 42.29
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-290432/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAF77387
                                                                                                                                                                                                                                                                                                                                                                      WO200121775-A1
                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB81022;
                                                                                                                                                                                               Pept1de
                                                                                                                                                                                                                                                         Protein
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AAB81022
                        NAME OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a mouse secretory type phospholipase A2 (PLA2) protein. The mouse secretory type PLA2-like protein can be used for screening in the development of inhibitors against the function of the protein. The present sequence represents mouse secretory type PLA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DWCCHAHDCCYQELFDQGCHPYVDHYIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnerary; antilnflammatory; tranquilliser; antiasthmatic; antiallergic; trauma; antirheumatic; antiarthritic; septic shock; pancreatitis; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New gene encoding mouse secretory type phospholipase A2 (PLA2) for screening for inhibitors of {\sf PLA2} -
                                                                                                                                                                                                                                                                                                                                                                            Mouse; secretory phospholipase A2; PLA2; screening; development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 142;
                                                                                                                                                                                                                                                                                                                Mouse secretory type phospholipase A2 protein SEQ ID NO:15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.8%; Score 313.5; DB 21; Length 42.2%; Pred. No. 1.7e-21; Live 20; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine phospholipase A2 (PLA2) amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 13-14; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LMN--OTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB12810 standard; Protein; 142 AA
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121 NLDSYNKRLRYYWRPRCKGKTPAC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98JP-0349604.
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                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-485554/43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAA73130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP2000166568-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                         27-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                              Inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                     AAB12810;
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                                                                                     RESULT 10
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lambda sPLA2-6.
                                                                                                                                                                                                                                                                  23-AUG-1988;
                                                                                                                                                                                                                                                                                               16-AUG-1988;
                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        Johnson LK,
                                                                                                                                                                                                        WO8901773-A.
                                                                                                                                                                                                                                     09-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP93112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sednence
                                                                                                                                                                             Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP9311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to human secretory phospholipase A2 (PLA2) protein and the gene encoding it. Inhibitors of phospholipase A2 have antibacterial; immunosuppressive; antiinflammatory; tranquilliser; vulnerary; antiasthmatic; antiallargic; antirheumatic; and antiarthritic activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in the diagnosis of PLA2 associated diseases e.g. septic shock, adult respiratory distress syndrome, pancreatitis, trauma, bronchial asthma, allergic rhinitis and rheumatoid arthritis. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secretory phospholipase A2 and encoded gene, useful in diagnosis of and screening drug candidates for treating associated diseases e.g. septic shock, adult respiratory distress syndrome and rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 HPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLMNQ--TYREEYRGFLNVY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnerary; antinflammatory; tranquilliser; antiasthmattc; antiallergic; trauma: antirheumatic; antiarthritic; septic shock; pancreatitis; human; adult respiratory distress syndrome; ARDS; bronchial asthma; allergic rhinitis; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 GSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCCHAHDCCYQELFDQGC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.3%; Score 309; DB 22; Length 142; 43.8%; Pred. No. 4.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
   Human phospholipase A2 (PLA2) amino acid sequence.
                                                                                                                                                                                                  20..142
/label= Mature_PLA2
/note= "Mature phospholipase A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Mismatches
                                                                                                                                                                     1..19
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 46-47; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP93363 standard; protein; 144 AA.
                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             Suzuki N, Hanasaki K;
                                                                                                                                                                                                                                                                                                                    18-SEP-2000; 2000WO-JP06344
                                                                                                                                                                                                                                                                                                                                                 99JP-0266616
                                                                                                                                                                                                                                                                                                                                                                              (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represents human PLA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-290432/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 AA;
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                                                                                                                                                                                                                                                             WO200121775-A1
                                                                                                                                                                                                                                                                                                                                                   21-SEP-1999;
                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                             Ishizaki J,
                                                                                                                                                                                                                                                                                           29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arthritis
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                                                                                                                                                                       Peptide
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clone lambda SPLA2cDNA-4 is one of four clones identified when probe oligo 2905 (AAN91257) was used to screen a cDNA library constructed from polyA+ message from a peritoneal cell RNA. It encodes the entire SPLA2 type A sequence which is given here. The mature peptide sequence (see FT) has a calculated molecular weight of 13,919 daltons. The same
                                       cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DRCCVTHDCCYKRLEKRGCGTKFLSYKFS-NSGSRITCA--KQDSCRSQLCECDKAAATC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalian synovial phospholipase A2- used in food processing design and screening of inflammation inhibitors, as an anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.6%; Score 302.5; DB 10; Length 144; 38.8%; Pred. No. 1.8e-20; Live 24; Mismatches 61; Indels 5;
                                       Human synovial phospholipase type A2 (sPLA2) as encoded by lambda SPLA2conA-4 and by the exons of clone lambda SPLA2-6.
                                                                                                                  Human synovial phospholipase A2; clone lambda sPLA2cDNA-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vada P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pruzanski W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88US-0231865, US-089883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 LMNQ--TYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 FARNKTTYNKKYQYYSNKHCRGSTPRC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOT-) BIOTECHN RES PARTN (UTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP93112 standard; Protein; 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPLA2-6 (AAN91260) in Figure 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drug or vaccine adjuvant etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                             88WO-US02896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAN91258, AAN91260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seilhamer JJ,
27-JUN-1980 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1989-085394/11
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Best Local Similarity
Matches 57; Conserv
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DB 10; Length 144;

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Acid stable phospholipase A2 - used for prodn. of antibodies and in the treatment or diagnosis of inflammation of diseases.
Inflammation; acid stable; phosphatide 2-acylhydrolase; lipolytic; glycerophospholipids; non-pancreatic.
                                                                                                                                      /note="calcium binding loop"
                                                                                                                                                   /note="calcium binding
                                 Location/Qualifiers
                                                                                                                                                                                                                                                      Kramer RM, Pepinsky RB, Hession C;
                                                          "Claim 12"
                                                                       /note- "Claim 14"
                                                                                                                                                                                                                                                                                                         Claim 44; Fig 12; 84pp; English.
                                             /label= signal
                                                                               /label= exon_1
                                                                                                      63..98
/label- exon_3
                                                                                                /label- exon_2
                                                                                                                         /label- exon_4
                                                                                                                                                                                                                89WO-US01418.
                                                                                                                                                                                                                              88US-0181893
                                                                                                                                                                                                                                                                        N-PSDB; AAN91825, AAN97209.
                                                                                                                                                                                                                                          (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                  WPI; 1989-324225/44
                   Homo sapiens.
                                                                                                                              Binding-site
                                                                                                                                           Binding-site
                                                                                                                                                                                                                11-APR-1989;
                                                                                                                                                                                                    19-0CT-1989.
                                                                                                                                                               Active-site
                                                                                                                                                                           Active-site
                                                                                                                                                        Active-site
                                                                                                                                                                     Active-site
                                      Peptide
                                                   Peptide
                                                                Peptide
                                                                                                     Region
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The protein sequence was deduced from a DNA sequence obtd, from a genomic DNA library which was prepd. from a mutant fibroblast cell genomic DNA library which was prepd. from a mutant fibroblast cell allowable to a the which contains 5 copies of the x chromosome (GM5009). The style allowable to be incomplete at the N-terminal since no promoter-like sequences are found in the DNA within 100 nucleomature protein confirmed results obtd. by direct sequencing of the mature protein confirmed results obtd. by direct sequencing of the putified protein. This sequence represents an amphiphilic alphateristic putified protein. This sequence represents an amphiphilic alphateristic putified protein of PLA_2 mols. It has highly conserved lipophilic residues (e.g. Leu (25), phe (25), and lie (29) and there is a cluster of basic amino acids (e.g. Arg (27), Lys (30) and Lys (35)] of PLA_2. There is a characteristic stretch of residues which complises part of the calcium binding loop: Tyt(4)-cly-cys-x-cys-wich constitute the acitive site (see features) are also present, and the protein exhibits the placement of half-cysteine residues typical of a Gp II PLA_2, having a Cys residue at position 70 and a half cysteine at the C-terminal. (The consensus sequence was and C. array wonom atrox venom.

144 AA;

Sequence

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61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                               Human growth hormone; granulocyte-colony stimulating factor; G-CSF;
phospholipase A2; HGH; PCR; polymerase chain reaction; gene therapy;
erythroid cells; cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is encoded by the phospholipase A2 (PLA2) CDNA. The CDNA was amplified using the primer sequences given in AAQ26370-1 by PCK from a human lung cDNA library. The CDNA sequence was used in promoter and a dominant control region. This vector was used in a expression system comprising a mammalian cell transformed with the vector. This expression system could be used to prepare bharmacologically useful polypeptides eg. human growth hormone (HGH), granulocyte-colony stimulating factor (G-CSF) and PLA2, and for gene therapy. The mammalian host comprises erythroid cells and a
                                           Gaps
                                                                1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRCQPKDEV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression vectors for use in mammalian cells - contain dominant control region derived from beta-globin gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uuery Match 31.6%; Score 302.5; DB 13; Length 144;
Best Local Similarity 38.8%; Pred. No. 1.8e-20;
Matches 57; Conservative 34. wi. .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grosveld FG, Hollis M, Needham MRC;
                                         61; Indels
    31.6%; Score 302.5; DB 10
38.8%; Pred. No. 1.8e-20;
tive 24; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Mismatches
                                                                                                                                                                                            121 LMNO--TYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                              118 FARNKTTYNKKYQYYSNKHCRGSTPRC 144
                                                                                                                                                                                                                                                                                                      AAR25416 standard; Protein; 144 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ICIL ) IMPERIAL CHEM IND PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91GB-0026984.
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Query Match
Best Local Similarity 38.8%
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                     06-JAN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antoniou M, Gooding C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heterologous promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ26372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-DEC-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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- 1 MKTLLLLAVIMIFGLLQAHGNLVNFHRMIKLTJGKEAALSYGFYGCHCGVGGRGSPKDAT 60
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121 LMNQ--TYREEYRGFLNVYCOGPTPNC 145 || ::| : | :| | | | 118 FARNKTTYNKKYOYYSNKHCRGSTPRC 144 q

Search completed: February 10, 2003, 10:36:32 Job time : 38 secs

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February 10, 2003, 10:35:31; Search time 15 Seconds (without alignments) 329.537 Million cell updates/sec
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! /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
! /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
! /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
! /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
! /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
}: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                   262574 segs, 29422922 residues
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Gapop 10.0 , Gapext 0.5
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957
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	Description	•	, ,	, ,	Sequence 3/, Appl	,	4	4	Sequence 35, Appl	35,	35,	Seguence 3, Appli	θ,	-	5	, ,	* <	, (, , ,	, c	ν, ν, ι	32,	32,		30	200	200	Š,	ì,	H	Sequence 43, Appl	
SUMMARIES	ΩI	US-08-186-895-10	US-08-888-407-37	US-06-362-37	PCT-11SQ4-07926-37	0.056.01.00.00	/TC-006-00 CO	118-08-469-407-21	764-00-00 50	200-200-300-300-300	26/0-8694-073			US-08-888-497-42			US-08-170-360-4	US-08-888-497-3	US-09-362-230	PCT-US94-07926-	CC-08-888-70-511	5-164-000-00	95-60-50	PCI - 0294	US-08-888	us-09-362	PCT-US94-	115-08-966-317-1	71C 00C 00 CD	I-0//-69#-60-co	US-U8-888-497-43	
	Length DB	4	144 2	4	144 5	٠.	146	·												124 5						~	7	S	165.4		5	
di	Query Match Le	31.6	31.6	31.6	31.6	30.8	8.06	30.1	30.1	30.1	1000		0.0	29.0	29.0	29.0	28.8	28.8	28.8	28.8	28.8	28.6	9 0	Э С	7.97	28.1	28.1	28.1	28.1	,		
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4 US-09-362-230-43 2 US-08-888-497-22 4 US-09-362-230-22 5 PCT-US94-07926-22 2 US-08-888-497-40 4 US-09-09-362-230-40 5 PCT-US94-07926-40 1 US-09-170-360-5 1 US-08-170-360-5 1 US-08-170-360-5 2 US-08-888-497-44 5 PCT-US94-07926-44 1 US-09-170-360-1 1 US-07-174-534A-1 2 US-08-1888-497-34 4 US-09-362-230-34 5 PCT-US94-07926-34	ALIGNMENTS US/08186895 11 vyn iaurice R.C. Tare Franklin G. Expression Systems 10 obrby & Cushman et, N.W. C-DOS/WS-DOS Release #1.0, Version #1.25 TA: US/08/186,895 -1994 US/08/046,383 -1993 US/08/046,383 -1993 N. 16,773 BER: PW:/3893/93802/MJW AMATION: N. 16,773 BER: N. 16,773 16,773 16,773 16,773 16,773 1700: 18,773 18,	%; Score 302.5; DB 1; %; Pred. No. 8.9e-22; 24; Mismatches 61;
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77777777777777777777777777777777777777	-10 Applica Applica FORMATIO T: Needi T: Good: T	imilarity ; Conser
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Patent No. 635204.

GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seithamer, Jeffrey J.
APPLICANT: Seithamer, Jeffrey J.
APPLICANT: Seithamer, Jeffrey J.
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
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61 DRCCVTHDCCYKRLEKRGCGTKFLSYKFS-NSGSRITCA--KQDSCRSQLCECDKAAATC 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
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APPLICATION NUMBER: US/09/362,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US 08/097,354
                                                                   121 LMNQ -- TYREEYRGFLNVYCQGPTPNC 145
                                                                                                         118 FARNKTTYNKKYQYYSNKHCRGSTPRC 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
                                                                                                                                                                                                                   Sequence 37, Application US/09362230 Patent No. 6352849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: INZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
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APPLICATION NUMBER: US 08
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Manso, Peter J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 200 East Divi
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APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
ONUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
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                                                                                                                    61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                                        61 DRCCVTHDCCYRRLEKRGCGTKFLSYKFS-NSGSRITCA--KQDSCRSQLCECDKAAATC 117
                                                              1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.6%; Score 302.5; DB 2; Length 144; 38.8%; Pred. No. 8.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Mismatches
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Fort Lauderdale
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                                                                                                                                                                                                            121 LMNQ--TYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/888,497
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Patent No. 5972677
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IBM PC compatible
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INFORMATION FOR SEQ ID NO: 37:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Manso, Peter J. REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-527-2498
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                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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CLASSIFICATION:
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                                                                         APPLICANT: Tiscifield, Jay A.
APPLICANT: Tiscifield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DRCCVTHDCCYKRLEKRGCGTKFLSYKFS-NSGSRITCA--KQDSCRSQLCECDKAAATC 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 31.6%; Score 302.5; DB 5; Length 144; Best Local Similarity 38.8%; Pred. No. 8.9e-22; Matches 57; Conservative 24; Mismatches 61; Indels 5,
                                                                                                                                                                                                                                      ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: PCT/US94/07926
15-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                       Sequence 37, Application PC/TUS9407926
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 LMNQ--TYREEYRGFLNVYCQGPTPNC 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFRENCE/DOCKET NUMBER: IN21(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
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Patent No. 6103469
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-
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INFORMATION FOR SEQ ID NO: 37:
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LENGTH: 144 amino acids
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                                                                                                                                                                                                                                                                                                                                                       ZIP: 33301
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE;
                    PCT-US94-07926-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-966-317-4
RESULT 4
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66 AHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMYLCLM--N 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.8%; Score 294.5; DB 3; Length 146; 42.3%; Pred. No. 5.2e-21; tive 20; Mismatches 55; Indels 7;
                APPLICANT: Shah, Purvi
APPLICANT: COTLEY, Neil C.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,317
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                               ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF-0403 US TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09489770; Patent No. 6399301
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R. APPLICANT: Guegler, Karl J. APPLICANT: Shah, Purvi. APPLICANT: Shah, Purvi. APPLICANT: CORIEY, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 146 amino acids
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MEDIUM TYPE: Diskett
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Matches 60; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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; CLONE: 204319
US-08-966-317-4
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                                                                                                                                                                                                                  94304
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              APPLICANT:
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                                                                                                                                                                                             COUNTRY:
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US-09-489-770-4
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CLASSIFICATION:
                                                                  FILING DATE:
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US-09-362-230-35
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 AHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNNVLCLM--N 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 THDCCYNRLEKRGCGTKFLITKFSYRGG-QISCS-TNQDSCRKQLCQCDKAAAAECFARNK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 VAILA-GSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCCH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 VVIMAFGSI -- QVQGSLLEFGQMILFKTGKRADVSYGFYGCHCGVGGRGSPKDATDWCCV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 30.8%; Score 294.5; DB 4; Length 146; Best Local Similarity 42.3%; Pred. No. 5.2e-21; Matches 60; Conservative 20; Mismatches 55; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/489,770
                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0403 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/966,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 KSYSLKYQFYLNKFCKGKTPSC 146
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 650-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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LIBRARY: GenBank
CLONE: 204319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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Palo Alto
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US-09-489-770-4
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                                         COUNTRY:
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               STATE:
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APPLICANT: Tischfield, Jay A.
APPLICANT: Sellhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 AHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNNVLCLM--N 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 THDCCYNRLEKRGCGTKEVTYKFSYRGG-QISCS-INQDSCRKQLCQCDKAAAAECFARNK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 VAILA-GSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCCH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.1%; Score 288.5; DB 2; Length 1441.5%; Pred. No. 2e-20; tive 20; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.25
                  Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 200 East Broward Boulevard
Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/09/362,230
                                                                                                                                                                                                                                                                                                            IN21044-5
                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
                                                                APPLICATION NUMBER: US/08/888,497
                                                                                                                                                                                                  US 08/097,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 35, Application US/09362230 Patent No. 6352849 GENERAL INFORMATION:
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 KSYSLKYQFYPNKFCKGKTPSC 146
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: IN:
TELECOMMONICATION INFORMATION:
TELEPHONE: 305-527-2498
                                                                                                                                                                                                                    FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J
REGISTRATION NUMBER: 32,264
                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 146 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 41.5%
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 305-72,
TELEPHONE: 305-764-4996
                                           CURRENT APPLICATION DATA:
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                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                   CLASSIFICATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tilechfield, Jay A.
APPLICANT: Selihamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amile Acid Sequences
TITLE OF INVENTION: Sequences Tebby, Antisense Sequences and Nucleotide
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 AHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM--N 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.1%; Score 288.5; DB 4; Length 146;
41.5%; Pred. No. 2e-20;
atlve 20; Mismatches 56; Indels 7; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 VVIMAFGSI--QVQGSLLEFGQMILFKTGKRADVSYGFYGCHCGVGGRGSPKDATDMCCV 66
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STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
                                                                 APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATOOMEL NEWEL 26-JUL-1993
NAME: MANBO, PECET J.
REGISTRATION NUMBER: 32,264
REFERNCE/CDOCKET NUMBER: IN21044-5
TELEPHONE: 305-527-249
TELEPHONE: 305-577-249
TELEPHONE: 305-577-249
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-7UL-1993
ATTONNEY/AGENT INFONMATION:
NAME: MAISO, PECEN J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: PCT/US94/07926
15-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                  146 amino acids
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MEDIUM TYPE: Floppy of
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Best Local Similarity
Matches 59; Conservē
                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                              FILING DATE:
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                                                                                                                                                                                                                                                                                                                  LENGTH:
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66 AHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM--N 123
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                                                                                                                                                                                                                                                                                        7; Gaps
                                                                                                                                                                                                                                                                                                                      7 VAILA-GSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCCH 65
                                                                                                                                                                                                                                                                                                                                                 30.1%; Score 288.5; DB 5; Length 146; 41.5%; Pred. No. 2e-20; Live 20; Mismatches 56; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3. Application US/08966317
Patent No. 6103469
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: Filed Herewith
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              TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INPORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07926-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 QTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 KSYSLKYQFYPNKFCKGKTPSC 146
TELECOMMUNICATION INFORMATION: TELEPHONE: 305-527-2498
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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Matches 59; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: Filed H
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CITY: Palo Alto
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REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN
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TELEPHONE: 305-527-2498
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Best Local Similarity
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US-08-888-497-42
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                                                                                                                                                                9 ILAGSVLS----TAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCC 64
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                                                                          29.6%; Score 283; DB 3; Length 146; 37.1%; Pred. No. 6.6e-20;
                                                                                                            56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
APPLICANT: HUMAN PHOSPHOLIPASE A2 PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/489,770
                                                                                                              26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09489770 Patent No. 6399301 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      123 NQTYREEYRGFLNVYCQGPTPNC 145
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NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
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TELEPHONE: 650-855-0555
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER REMANBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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                                                                                               Best Local Similarity 37.1
Matches 53; Conservative
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CLONE: 984837
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Best Local Similarity
Matches 53; Conserv
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LIBRARY: Generate 984837
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                                                                                                                                                                                                                                                                                                                                                                                             US-09-489-770-3
                                             US-08-966-317-3
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                                                                                 Query Match
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GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SLLEFGOMILFKTGKRADVSYGFYGCHCGVGGRGSPKDATDWCCVTHDCCYNRLEKRGCG 60
                                                                                                                                                     66 VTHDCCYKSLEKSGCGTKLLKYKXSHQGG-QITCS-ANQNSCQKRLCQCDKAAAECFARN 123
                                                                                                                65 HAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM-- 122
                                           9 ILAGSVLS----TAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.0%; Score 278; DB 2; Length 125; 41.7%; Pred. No. 1.7e-19; tive 18; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 East Broward Boulevard
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FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 42, Application US/08888497 Patent No. 5972677
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RESULT 15
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                                                                                                                                                                                                                             APPLICANT: Tischfield, Jay A. APPLICANT: Tischfield, Jay A. APPLICANT: Sellhamer, Jeffrey J. TITLE OF INVENTION: Mammallian Phospholipase A2 Nucleotide TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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61 TKFVTYKFSYRGG-QISCS-TNQDSCRRQLCQCDRAAAECFARNKKSYSLKYQFYPNKFC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 PYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM--NQTYREEYRGFLNVYC 138
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                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 08/097,354
                                                                                                                                                                       Sequence 42, Application US/09362230
Patent No. 6352849
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: INTELECOMMUNICATION INFORMATION: TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 26-JUL-1993
ATTORNEY/ACENT INFORMATION:
NAME: Manbo, Peter J.
REGISTRATION NUMBER: 32,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
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APPLICATION NUMBER:
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Best Local Similarity
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                                      139 QGPTPNC 145
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                                                                           119 KGKTPSC 125
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119 KGKTPSC 125
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                                                                                                                                                     US-09-362-230-42
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APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 PYVDHYDHTIENNTEIVCSDLNKTECDKOTCMCDKNMVLCLM--NOTYREEYRGFLNVYC 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 29.0%; Score 278; DB 5; Length 125; Best Local Similarity 41.7%; Pred. No. 1.7e-19; Matches 53; Conservative 18; Mismatches 52; Indels
                                                                                                                                                                                                                                                             ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
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Patent No. 5656602
GENERAL INFORMATION:
APPLICANT: Tseng, Albert P. S.
APPLICANT: Inglis, Adam
TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: MANSO, PELER J.
REGISTRATION NUMBER: 32,264
REFERRNCE/DOCKET NUMBER: IN21044-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US94/07926
FILING DATE: 15-JUL-1994
                              Sequence 42, Application PC/TUS9407926 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          STREET: 200 East Brown CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                       USA
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PCT-US94-07926-42
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81 PYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLMNQ--TYREEYRGFLNVYC 138
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28.8%; Score 275.5; DB 1; Length 124;
Best Local Similarity 39.4%; Pred. No. 2.8e-19;
Matches 50; Conservative 21; Mismatches 51; Indels 5
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
CITY: Washington
COWTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,360
FILING DATE: 03-MAR-1994
CLASSIFICATION NUMBER: MAP-1994
CLASSIFICATION NUMBER: AD PCT/AU92/00333
FILING DATE: 06-JUL-1992
PRIOR APPLICATION NUMBER: AD PX 7058
FILING DATE: D6-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Ernsk Barbara G.
REFERENCE/DOCKET NUMBER: 1871-104A
TELECOMMUNICATION INFORMATION:
NAME: Ernsk DATON
REFERENCE/OCKET NUMBER: 1871-104A
TELECOMMUNICATION NOW 4:
SEQUENCE CHARACTERISTICS:
FUNCHALION FOR SEQ 1D NO: 4:
SEQUENCE CHARACTERISTICS:
FUNCHALION FOR SEQ 1D NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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February 10, 2003, 10:37:16 ; Search time 11 Seconds (without alignments) 338.586 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Published_Applications_AA:*

Database :

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14: /cgn2_6/ptodate/2/pubpaa/USO0_PUBCOMB.pep:*

SUMMARIES

Description		Sequence I/, Appl	Sequence 6, Appli	Sequence 1010, Ap		Æ,	Sequence B, Appli	Sequence 534, App	Sequence 534, App	Seguence 534, App	Sequence 534, App	4	Triddy // Domontoo	riddy ' Political of Applit	seduence 5, Appli	Sequence 5, Appli	Sequence 511, App		- (Sednence In, Appl	Sequence 873, App	Sequence 14, Appl
ID	113-00-040-204-17	115-00-835-006A-6	US-09-935-996A-6	US-10-134-F01-4	118-10-124-391-4	118-00-003-000-0	11S-10-000-01-01	118-10-121-040-624	100 100 101 01 101	US-IO-IZ3-904-534	US-10-140-470-534	0S-06-66-60-80	US-10-124-591-1	US-09-987-57-5	C C C C C C C C C C C C C C C C C C C	02-03-30/-000-0	US-09-925-297-511	US-09-993-999-7	01-000-200-50	01 100 100 00	02-03-322-237-873	US-09-975-374A-14
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Query Match	36,9	36.8	31.6	30	29.6	29.6	28.6	28.6	28.6		0 0	28.5	28.1	27.6	27 6			8.T7	21.3	a VI	, ,	13./
Score	353	352	302.5	294.5	283	283	273.5	273.5	273.5	273 5		6.212	268.5	264.5	264.5	220 5	200	208.5	203.5	7415	10.1	101
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RESULT 2

Sequence 211, App Sequence 290, App Sequence 2, Appl 1 Sequence 2, Appl 1 Sequence 2, Appl 1 Sequence 3, Appl 1 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 15, Appl 1 Sequence 15, Appl 1 Sequence 15, Appl 1	Polypeptides, and Antibodies	Length 145; Indels 8; Gaps 4; CYCGLGGRGOPKDEVDW 62 :
10 US-09-764-898-211 10 US-09-781-100-2 9 US-10-176-758-290 9 US-10-175-737-290 9 US-10-175-738-290 9 US-10-175-738-290 9 US-10-175-752-290 9 US-10-175-752-290 9 US-10-176-757-290 9 US-10-176-757-290 9 US-10-176-757-290 9 US-10-176-757-290 10-10-180-552-290 10-10-180-552-290 10-10-180-552-290 10-10-180-552-290 10-10-180-552-290 10-10-180-552-290 10-10-180-552-290 10-10-180-552-290 10-10-180-552-290 10-10-180-552-290 10-10-180-552-290 10-10-180-552-290 10-10-180-552-290 10-10-180-552-290 10-10-180-552-290 10-10-180-552-290 10-10-180-552-290 10-10-180-552-290 10-10-10-10-10-10-10-10-10-10-10-10-10-1	ALIGNMENTS 9384 Polynucleotides, 09/969,384 31/10542 6,384 4,118	ch 36.9%; Score 353; DB 9; Length 145; 1 Similarity 45.5%; Pred. No. 1.4e-25; 66; Conservative 19; Mismatches 52; Indels 8; G ALLAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGOPKDEVDW ALLCGLVWAGVIPIGGGILNLNKMVKQVTGKMPILSYWPYGCHGGGRGOPKDATDM CHAHDCCYOELFDOGCHPYVDHYDHTIENVTEIVCSDLNKTECDKQTCMCDKNNVLCLM
92.5 9.7 604 1 90.5 9.5 9.7 604 1 90.5 9.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 9.5 1523 9 90.5 90.5 90.5 90.5 1523 9 90.5 90.5 90.5 90.5 90.5 90.5 90.5 90	17 Application US/C NEWATION: MOOFE, et al. WENTION: Human Ge NGE: PTOS5P1 LICATION NUMBER: LAING DATE: 2001-04-0 GATE: 2000-09-2 CATION NUMBER: 60 CATION	tch 1 Similarity 66. Conservat ANILAGSVLSTA 11: LALLCGLVVMAGVIPI CCHAHDCCYOELFDOG CCOTHDCCYDHLKTQG
01102222222222222222222222222222222222	RESULT 1 US-09-969-384. ; Sequence 17; Publication ; GENERAL INFC APPLICANT; TILE OF IN ; FILE REFERIN ; CURRENT APF CURRENT FILI ; PRIOR APPLI ; PRIOR FILLI ; PRIOR APPLI ; PRIOR FILLI ; SOFTWARE: P ; SOFTWARE: P ; SOFTWARE: P ; TYPE: PRI ; TYPE: PRI ; TYPE: PRI ; TYPE: PRI ; ORGANISM:	Query Mar Best Loca Matches Qy 7 7 9 0b 3 1 Qy 63 Q Qy 63 Q Qy 63 Q Qy 63 Q Qy 123 P

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM FILE REFERENCE: 28110/35915A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 36.8%; Score 352; DB 10; Length 145; Best Local Similarity 45.5%; Pred. No. 1.7e-25; Matches 66; Conservative 19; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Steve Ruben TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/835,996A CURRENT FILING DATE: 2001-04-16
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PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-10-18
PRIOR PILING DATE: 2000-09-22
PRIOR PLILCATION NUMBER: US 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/197,137
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          Sequence 6, Application US/09835996A Patent No. US20020142953A1
                                                                         APPLICANT: Ballinger, Dennis
APPLICANT: Loeb, Debra
APPLICANT: Montgomery, Julie
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
                                                                                                                                                                              Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
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Drmanac, Radoje
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Wanq, Dunrui
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                                                                                                                                                                                                                                                                                                           Ren, Feiyan
                                                                                                                                                                                                                                           Zhao, Qing
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                                                            GENERAL INFORMATION:
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US-09-835-996A-6
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                                                                                                                                                                                                                                1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                                                                        31.6%; Score 302.5; DB 10; Length 164; 38.8%; Pred. No. 6.7e-21; Live 24; Mismatches 61; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corley, Neil C.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPOTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEO for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0403 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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APPLICATION NUMBER: US/10/124,591
FILING DATE: 16-Apr-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/489,770
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APPLICATION NUMBER: 08/966,317
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                            121 LMNQ--TYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                    138 FARNKTTYNKKYQYSNKHCRGSTPRC 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 146 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-124-591-4
; Sequence 4, Application US/10124591
; Patent No. US-20020177208A1
; GENERAL INFORMATION:
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Guegler, Karl J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1010
LENGTH: 164
                                                                                                                                                         Query Match
Best Local Similarity 38.89
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
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                                                                                        ; ORGANISM: Homo sapiens
US-09-925-300-1010
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                                                                      TYPE: PRT
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Gerritsen, Mary E.
Goddard, Audrey
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mus musculus US-09-993-999-8
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APPLICANT:
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                                                                                               7 VAILA-GSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYGGLGGRGQPKDEVDWCCH 65
                                                                                                                 Gaps
                                30.8%; Score 294.5; DB 9; Length 146; 42.3%; Pred. No. 3.2e-20; tive 20; Mismatches 55; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 29.6%; Score 283; DB 9; Length 146; Best Local Similarity 37.1%; Pred. No. 3.6e-19; Matches 53; Conservative 26; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corley, Neil C.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEX for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,591
FILING DATE: 16-Apr-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PF-0403 US TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/489,770
FILING DATE: «CHRIOWIN-
APPLICATION NUMBER: 08/966,317
FILING DATE: «CUNKNOWIN-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hawkins, Phillip R. Bandman, Olga Guegler, Karl J. Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10124591; Patent No. US20020177208A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                      124 OTYREEYRGFLNVYCOGPTPNC 145
                                                                                                                                                                                                                                                         125 KSYSLKYQFYLNKFCKGKTPSC 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: GenBank
CLONE: 984837
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                            Query Match
Best Local Similarity
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                                                                60;
US-10-124-591-4
                                                                                                                                                                                                                                                                                                                                          US-10-124-591-3
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                                                                Matches
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65 HAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM-- 122
                                                                                                         9 ILAGSVLS----TAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCC 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.6%; Score 283; DB 10; Length 146;
37.1%; Pred. No. 3.6e-19;
itive 26; Mismatches 56; Indels 8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 ILAGSVLS----TAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCC 64
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APPLICANT: HO, I-Cheng
APPLICANT: Arm, Jonathan P.
APPLICANT: Austen, K. Frank
APPLICANT: Austen, K. Frank
APPLICANT: Glincher, Laurie H.
TITLE OF INVENTION: Expressed in Th2 Cells
TITLE OF INVENTION: Expressed in Th2 Cells
FILE REFERENCE: HUI-046
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: 60/246,316
PRIOR APPLICATION NUMBER: 2000-11-06
PRIOR FILING DATE: 2000-11-06
NUMBER OF SEQ ID NOS: 19
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Best Local Similarity 37.18; Pred. No. .....
Matches 53; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Sequence 534, Application US/10028072; Publication No. US20030004311A1; GENERAL INFORMATION:
                                                                                                                                                                   123 NQTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                             Sequence 8, Application US/09993999
; Patent No. US20020110891A1
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CURRENT APPLICATION NUMBER: US/10/028,072 CURRENT FILING DATE: 2001-12-19
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PRIOR APPLICATION NUMBER: 60/059836
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-24
PRIOR FILING DATE: 1997-09-24
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/06285
PRIOR PELICATION NUMBER: 60/06287
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063816
PRIOR PELING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
PRIOR PELING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
PRIOR PELING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063045
PRIOR PELING DATE: 1997-10-27
PRIOR PELING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063786
PRIOR APPLICATION NUMBER: 60/0637876
PRIOR APPLICATION NUMBER: 60/0637876
PRIOR APPLICATION NUMBER: 6
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FILING DATE: 1997-11-12
APPLICATION NUMBER: 60/065846
FILING DATE: 1997-11-17
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PRIOR APPLICATION NUMBER: 60/066364
                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
                                                                                                                                                                                                                CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
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APPLICATION NUMBER: 60/059263
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APPLICATION NUMBER: 60/059184
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                       Watanabe, Colin K
Wood, William
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Tumas, Daniel
                                                                                                                              LITLE OF INVENTION:
                                                                                                   Zhang
                                                                                                                                                      FILE REFERENCE:
                                                             APPLICANT:
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PRIOR APPLICATION NUMBER: 66/066511
PRIOR FILING DATE: 1997-11-24
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PRIOR PELLING DATE: 1997-11-24
PRIOR PELLING DATE: 1997-11-24
PRIOR PELLING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 66/069212
PRIOR PILING DATE: 1997-12-11
PRIOR PELING DATE: 1997-12-11
PRIOR PELING DATE: 1997-12-11
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 66/069694
PRIOR PILING DATE: 1998-12-16
PRIOR PELING DATE: 1998-01-23
PRIOR PILING DATE: 1998-01-23
PRIOR PILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 66/074092
PRIOR PILING DATE: 1998-03-09
PRIOR PILING DATE: 1998-03-09
PRIOR PILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 66/07791
PRIOR PILING DATE: 1998-03-12
PRIOR PILING DATE: 1998-03-25
PRIOR PILING DATE: 1998-03-25
PRIOR PILING DATE: 1998-03-25 PRIOR APPLICATION NUMBER: 60/083322 PRIOR PILING DATE: 1998-04-28 PRIOR PLICATION NUMBER: 60/08345 PRIOR FILING DATE: 1998-04-29 PRIOR PILING DATE: 1998-04-29 PRIOR PILING DATE: 1998-05-07 PRIOR PLING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084627 DR FILING DATE: 1990-02.

R FILING DATE: 1998-03.

R FILING DATE: 1998-03-27

R APPLICATION NUMBER: 60/080165

R FILING DATE: 1998-03-31

R PLING DATE: 1998-04-09

R FILING DATE: 1998-04-09

R FILING DATE: 1998-04-09

R FILING DATE: 1998-04-09

R FILING DATE: 1998-04-09

R RILING DATE: 1998-04-14

SA APPLICATION NUMBER: 60/081695

DR FILING DATE: 1998-04-14

SA PELICATION NUMBER: 60/081817

OR APPLICATION NUMBER: 60/081817

OR APPLICATION NUMBER: 60/081817

OR APPLICATION NUMBER: 00/081818 PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
PRIOR PILING DATE: 1998-05-12 PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/086414 FILING DATE: 1998-05-22 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/082999 FILING DATE: 1998-04-24 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083545 PRIOR FILING DATE: 1998-05-13 PRIOR APPLICATION NUMBER: 60/085338 PRIOR FILING DATE: 1998-05-13 PRIOR APPLICATION NUMBER: 60/085339 APPLICATION NUMBER: 60/085704 APPLICATION NUMBER: 60/079663 FILING DATE: 1998-02-27 APPLICATION DATE: 1997-11-21
APPLICATION NUMBER: 60/066453
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/066511
FILING DATE: 1997-11-24 1998-05-13 1998-05-13 PRIOR PRIOR

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APPLICANT: "CAND, "CEMIN TELLICANT: "CAND, SERVENT SHOWN SERVENT STATE TO SERVENT SHOWN SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERBNCE: P3330R1C17 CURRENT APPLICATION NUMBER: US/10/121,049 CURRENT APPLICATION NUMBER: US/10/121,049 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550 SEQ ID NO 534 LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 CCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT APPLICATION DATE: 202-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                28.6%; Score 273.5; DB 9; Length 116;
42.9%; Pred. No. 2.1e-18;
ative 15; Mismatches 36; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 VAILAGSVLSTA----HGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGOPKDEVDW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 534
LENGTH: 116
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                        Stewart, Timothy A.
                                                                   APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Gerritsen, Mary E.
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Watanabe, Colin K
Wood, William
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Filvaroff, Ellen
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                                                 Tumas, Daniel
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ORGANISM: Homo Sapien
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US-10-123-904-534
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3 LALLCGLVVMAGVIPIQGGILNLNKMYKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW 62
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28.6%; Score 273.5; DB 9; Length 116;
Best Local Similarity 42.9%; Pred. No. 2.1e-18;
Matches 54; Conservative 15; Mismatches 36; Indels 21
                                                                               PRIOR FLLING DATE: 1938-00-18
PRIOR PILING DATE: 1938-06-04
PRIOR PILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-10
PRIOR PLING DATE: 1998-06-10
PRIOR PAPLICATION NUMBER: 60/08810
PRIOR PILING DATE: 1998-06-11
PRIOR PAPLICATION NUMBER: 60/08958
PRIOR PILING DATE: 1998-06-11
PRIOR PELING DATE: 1998-06-11
PRIOR PELING DATE: 1998-06-17
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PRIOR PELING DATE: 1998-06-19
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-26
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PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-07-01
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Publication No. US20030022239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Personary
                 R FILING DATE: 1998-05-22

R FILING DATE: 1998-05-22

R FILING DATE: 1998-05-28

R FILING DATE: 1998-05-08

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/08830

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/08871
APPLICATION NUMBER: 60/086430
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                              63 CCQTHDCCYDHLKTGGCGIYKDN------LMXSSIHCMDLSQRYC------LMANF 105
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7. VAILAGSVLSTA----HGSLLNLKAMVEAVIGRSAILSFVGYGGYGGLGGRGQPKDEVDW 62
                      28.6%; Score 273.5; DB 9; Length 116; 42.9%; Pred. No. 2.1e-18; tive 15; Mismatches 36; Indels 21;
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                                                                                                                                                                                                                                                                             Sequence 534, Application US/10140470
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                                                                                                                                                                                                                                                                                                Publication No. US20030022331A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerritsen, Mary E.
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Wood, William
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APPLICANT: Arm, Jonathan P.
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Gurney, Austin L.
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Gao, Wei-Qiang
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US-10-140-470-534
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61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                                                                                                                                                                                              28.5%; Score 272.5; DB 10; Length 137; 37.9%; Pred. No. 3.1e-18; tive 21; Mismatches 61; Indels 5;
APPLICANT: Austen, K. Frank
APPLICANT: Glimcher, Laurie H.
TITLE OF INVENTION: Phospholipase A2 Group Preferentially
TITLE OF INVENTION: Expressed in Th2 Cells
FILE REFERENCE: HUI-046
CURRENT APPLICATION NUMBER: US/09/993,999
CURRENT PAPLICATION NUMBER: 00/246,316
PRIOR FILING DATE: 2000-11-06
PRIOR PRIOR PILING DATE: 2000-11-06
NUMBER OF SEQ ID NOS: 19
SEQ ID NOS: 19
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corley, Neil C. TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,591
FILING DATE: 16-Apr-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF-0403 US TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/489,770 FILLING DATE: <Unknown>
APPLICATION NUMBER: 08/966,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hawkins, Phillip R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/10124591
; Patent No. US20020177208A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bandman, Olga
Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 LMNQ--TYREEYRGFLNVYC 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                      53; Conservative
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                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Mus musculus
US-09-993-999-9
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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Patent No. US20020169282A1

GENERAL INFORMATION:
APPLICANT: Canne, Lynne
APPLICANT: Simon, Reyna
TITLE OF INVENTION: Solid Phase Native Chemical Ligation of Unprotected or TITLE OF INVENTION: Solution
TITLE OF INVENTION: Solution
TITLE OF INVENTION: Solution
FILE REFERENCE: GREN-023/0110;
CURRENT APPLICATION NUMBER: US/09/987,675
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 09/097,094
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                      92 YTRAEBAGCSPKTERYSWQCVNQS-VLCGPA-ENKCQELLCKCDQEIANCLAQTEYNLKY 149
                                                                                                                                                                                                                                                                                        3; Gaps
                                                                                                                                                                                                                                                                                                                 11 AGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCCHAHDCC 70
                                                                                                                                                                                                                                                                                                                                     22 LLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCCHAHDCCYQELFDQGCHP 81
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                                                                                                                                                                                                                                    .ch 28.1%; Score 268.5; DB 9; Length 165; 1 Similarity 34.8%; Pred. No. 8.9e-18; 47; Conservative 23; Mismatches 62; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 27.6%; Score 264.5; DB 9; Length 118; 1 Similarity 41.2%; Pred. No. 1.4e-17; 49; Conservative 20; Mismatches 45; Indels 5
                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                   LENGTH: 165 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09987655; Patent No. US20020132975A1; GENERAL INFORMATION: APPLICANT: Canne, Lynne APPLICANT: Kent, Stephen B.H.
                      SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                      LIBRARY: OVARTUT01
CLONE: 816403
                                                                                                 TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 RGFLNVYCQGPTPNC 145
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                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                      Query Match
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APPLICANT: Simon, Reyna
TITLE OF INVENTION: Solid Phase Native Chemical Ligation of Unprotected or
TITLE OF INVENTION: N-Terminal Cysteine Protected Peptides in Aqueous
TITLE OF INVENTION: Solution
FILE REPRESENCE: GREN-023/01US
CURRENT APPLICATION NUMBER: US/09/987,655
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION UNBER: 09/097,094
NUMBER OF SEQ ID NOS: 6
SOCTION OF SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 YVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLMN--QTYREEYRGFLNVYC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 RTQSYRYRFAWGV-VTCEP--GPFCHVNLCACDRKLYYCLKRNLRSYNDQYQYFPNILC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 23.0%; Score 220.5; DB 10; Length 156;
1 Similarity 32.5%; Pred. No. 2.1e-13;
49; Conservative 23; Mismatches 60; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 EVDWCCHAHDCCYQE-----LFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQ 109
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27.6%; Score 264.5; DB 10; Length 118;
Best Local Similarity 41.2%; Pred. No. 1.4e-17;
Matches 49; Conservative 20; Mismatches 45; Indels 5;
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAJOS
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: CT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 511, Application US/09925297
Patent No. US20020081659A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 928
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-09-987-655-5
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-925-297-511
                                                                                                                                                                                                                                                                                                        LENGTH: 118
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SEQ ID NO 511
                                                                                                                                                                                                                                                                           SEQ ID NO 5
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Search completed: February 10, 2003, 10:41:12 Job time : 13 secs

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GenCore version 5.1.3

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 10:35:31; Search time 17 Seconds (without alignments)

Title: (without alignments)

950.034 Million cell updates/sec

Perfect score: 957
Sequence: 1 MKKFFTVAILAGSVLSTAHG.......EPPPEEVTCSHQSPAPPAPP 168
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum Match 0%
Maximum Match 0%
Maximum Match 0%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

	Description								phospholipase A2 (1pase			phospholipase a2 -		phospholipase A2 (pase			phospholipase A2 (a							phospholipase A2 (41
SUMMARIES	ID	.TC134.9		DAVATA	TABOR2	A 2 5 4 0 3	A33304	140004	CT0712	SC 200	000000	150098	T20098	770000	A44414 A54767	2074CA	TUCK!	751296	51000	20000	DEVIEN	F3V1AA T51380	121300 B5/763	70/100	151100	ם ל	7 -	322217	າຊ	509314	1
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	Length	138	144	122	145	146	146	146	138	137	122	138	146	13.0	130	138	138	138	3.0	138	1 20	138	158	121	124	123	9 6	122	3 6	122	! !
æ	Query		31.6	31.2	31.0	30.8	30.0	29.4	29.3	29.5	29.1	29.1	29.0	28.8	28.7	28.5	28.5	28.5	28.2	28.1	28.1	28.0	27.9	27.6	27.4	27.3	27.3	27.2	27.2	27.1	
	Score	309.5	302.5	298.5	297	294.5	287.5	281	280.5			278.5			275	272.5	272.5	272.5	269.5	269	268.5	267.5	267	264.5	262	61.	261.5	26	260	•	
	Result No.	1	7	e	4	S	Q	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	36	27	28	29	

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phospholipase
JC4877 D48188 A13900 A25806 PSRSBT 151381 PC4024 S33267 JX0480 JX05243 JC5243 S22388 A48188 PSRSB2
10000111000000001
137 122 122 122 138 138 121 121 125 125 121 121 121 121 121 121
0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0
258.5 258.5 259.5 251.5 251.5 250.5 250.5 250.5 250.5 249.5
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

phospholipase A2 (EC 3.1.1.4) precursor - halys viper C; Species: Agkistrodon halys (halys viper) C; Species: Agkistrodon halys (halys viper) C; Species: 09-0ct-1997 #sequence_revision 07-Nov-1997 #text_change 13-Nov-1998 C; Accession: 101342 Acta Biochim. Biophys. Sin. 28, 579-582, 1996 A; Title: Cloning of the BPLA2 gene from Agkistrodon halys Pallas. A; Title: Cloning of the BPLA2 gene from Agkistrodon halys Pallas. A; Contents: Snake venom A; Contents: Snake venom A; Contents: Snake venom A; Residues: 1-138 Apal. A; Residues: 1-138 Apal. A; Residues: 1-138 Apal. A; Residues: 1-138 Apal. A; Residues: He authors translated the codon GAC for residue 54 as Asn C; Comment: This protein catalyzes specifically the hydrolysis of the C-2 ester bond of C; Superfamily: phospholipase A2 C; Reywords: carboxylic ester hydrolase F; 1-16 /Domain: slonal sequence ## ## ## ## ## ## ## ## ## ## ## ## ##	Query Match Best Local Similarity 39.3%; Score 309.5; DB 2; Length 138; Best Local Similarity 39.5%; Pred. No. 1.8e-19; Matches 58; Conservative 26; Mismatches 52; Indels 11; Gaps 5; QY MKKFFTVAILAGSVLSTAHGSLLNLKANVEAVTGRSAILSFVGYGCYGGGGGRGPKDEV 60	RESULT 2 PSHUYF Phospholipase A2 (EC 3.1.1.4) IIA precursor [validated] - human Naflectrate names: phosphatidylcholine 2-acylhydrolase; placental PLA2; platelet-secr C;Species: Homo sapiens (man) C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 15-Sep-2000 C;Accession: A38862; B32862; A32847; A60263; A31350; pr0056; A32913; A60265; J; Biol. Chem. 264, 5768-5755, 1989 A;Title: Structure and properties of a human non-pancreatic phospholipase A-2. A;Reference number: A32862; MUID:89174633; PMID:2925633 A;Status: not compared with conceptual translation A;Molecule tyne- hum
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A; Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-ac A; Description: strongly enhanced when the phospholipid is condensed into a m A; Note: the reaction is strongly enhanced when the phospholipid is condensed into a m C; Superfamily: phospholipase A2 (S; Reywords: calcium; carboxylic ester hydrolase; homodimer; lipid degradation; metall C; Reywords: calcium; carboxylic ester hydrolase; homodimer; lipid degradation; metall C; Reywords: calcium; 75-86/Disulfide bonds: #status predicted F; 27, 29, 31, 48/Binding site: calcium (Tyr, Gly, Gly, Asp) #status predicted F; 47, 89/Active site: His, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Kini, R.M.; Kawabata, S.I.; Iwanaga, S. Toxicon 24, 117-1129, 1986
A;Title: Comparison of amino terminal region of three isoenzymes of phospholipases A2 A;Title: Comparison of amino terminal region of three isoenzymes of phospholipase, TFV PL-X. quence of the basic phospholipase, TFV PL-X. A;Reference number: A94320; MUID:87179112; PMID:3564060
                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene GBB:PLASG2A; PLA2B.
A;Gene GBB:PLASG2A; PLA2B.
A;Gene GBB:PLASG2A; PLA2B.
A;Cross references: GBB:120296; OMIM:172411
A;Gross references: GBB:120296; OMIM:172411
A;Map position: 1956-1-1p35
A;Introns: 14/1; 62/2; 98/1
C;Function: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-ac A;Description: catalyzes hydrolyses of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-ac A;Description: catalyzes hydrolase; extracellular protein; lipid degrada C;Keywords: andlcium; carboxylic ester hydrolase; extracellular protein; lipid degrada C;Keywords: andlcium; carboxylic ester hydrolase; extracellular protein; lipid degrada F;1-20/Domain: signal sequence #status predicted <SIG>F;1-144/Product: phospholipase A2 IIA #status experiment de AGF
F;21-144/Product: phospholipase A2 IIA #status experiment F;47,49,51,68/Ainding site: calcium (His, Gly, Asp) #status predicted F;67,111/Active site: His, Asp #status predicted
Teater, C.; Warrick, M.W.; Jones, N.D. submitted to the Brookhaven Protein Data Bank, May 1992
A;Reference number: A51043; PDB:1BBC
A;Reference number: A51043; PDB:1BBC
A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 21-144
A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 21-144
A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 21-144
Teater, C.; Warrick, M.W.; Jones, N.D.
Nature 352, 79-82, 1991
A;Title: Structure of recombinant human rheumatoid arthritic synovial fluid phospholi
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N.Alternate names: phosphatidylcholine 2-acylhydrolase
C.Species: Trimeresurus flavoviridis (habu)
C.Date: 30-Sep.1987 #sequence_revision 30-Sep-1987 #text_change 24-Apr-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
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A;Contents: annotation; X-ray crystallography
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tive 23; Mismatches 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LMNQ--TYREEYRGFLNVYCQGPTPNC 145
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A; Residues: 1-122 <KIN>
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A;Residues: 21-44 <GRE>
B;Wery, J.P.; Schevitz, R.W.; Clawson, D.K.; Bobbitt, J.L.; Dow, E.R.; Gamboa, G.; Goods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Parks, T.P.; Lukas, S.; Hoffman, A.F. Adv. Exp. Med. Biol. 275, 55-81, 1990
Ay:title: Purification and characterization of a phospholipase A-2 from human osteoarthri A; Reference number: A60265; MUID:91050835; PMID:2146857
A; Accession: A60265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-144 <CRO>
R; Lai, C.Y.; Wada, K.
Biochem. Biophys. Res. Commun. 157, 488-493, 1988
A; Title: Phospholipase A-2 from human synovial fluid: purification and structural homolo
A; Reference number: A31350; MUID:89076274; PMID:3202859
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A; Residues: 21-46, XX, 48-54 <HAR>
R; Residues: 21-46, XX, 48-54 <HAR>
R; Randa, A.; Ono, T.; Yoshida, N.; Tojo, H.; Okamoto, M.
B; Richem. Biophys. Res. Comnun. 163, 42-48, 1989
A; Title: The primary structure of a membrane-associated phospholipase A-2 from human spl
A; Reference number: A32913; MUID:89374261; PMID:2775276
A; Recession: A32913
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R;Crowl, R.; Stoner, C.; Stoller, T.; Pan, Y.C.; Conroy, R.
Adv. Exp. Med. Biol. 279, 173-184, 193-184
A;Title: Isolation and characterization of cDNA clones from human placenta coding for ph A;Reference number: A60263; MUID:91263879; PMID:1710870
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A; Molecule type: protein
A; Residues: 21.33 (IAI>
R; Hara, S.; Kudo, I.; Matsuta, K.; Miyamoto, T.; Inoue, K.
J. Blochem. 104, 326-328, 1988
J. Blochem. 104, 326-328, 1988
A; Reference number: PT0056; MUID: 89197814; PMID: 3240982
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                                                                                                                                                                                                                                                                       A; Title: Structure and properties of a secretable phospholipase A-2 from human platelets A; Reference number: A60266; MUID:91050834; PMID:2239446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-144 <KR3>
R; Sellhamer, J.J.; Pruzanski, W.; Vadas, P.; Plant, S.; Miller, J.A.; Kloss, J.; Johnson
B; Sellhamer, J.J.; Pruzanski, W.; Vadas, P.; Plant, S.; Miller, J.A.; Kloss, J.; Johnson
B. 1610. Chem. 264, 5335-5338, 1989
A; Title: Cloning and recombinant expression of phospholipase A-2 present in rheumatoid a
A; Reference number: A32847; MUID: 89174566; PMID: 2925608
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A; Residues: 21-40 < RREC>
Experimental source: adult articular cartilage
R; Green, J.A.; Smith, G.M.; Buchta, R.; Lee, R.; Ho, K.Y.; Rajkovic, I.A.; Scott, K.F.
Inflammation 15, 355-366, 1991
                                                                                                                                                                                                                                                R;Kramer, R.M.; Johansen, B.; Hession, C.; Pepinsky, R.B. Adv. Exp. Med. Biol. 275, 35-53, 1990
                                                                                                                                                                                                        A; Note: this protein was also detected in platelets
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A,Residues: 21-45,"X PARN
R:Recklies, A.D.; White, C.
Arthritis Rheum. 34, 1106-1115, 1991
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A; Residues: 1-144 <SEI>
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Arch. Biochem. Biophys. 331, 95-103, 1996
A:Title: Purlification and characterization of Ca(2+)-dependent phospholipases A(2) fr
A:Reference number: S71310; MUID:96268465; PMID:8660688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phospholipase A2 (EC 3.1.1.4) precursor (version 1) - rat
C; Species: Rattus norvegicus (Norway rat)
C; Date: 29-dan-1990 #sequence_revision 29-Jan-1990 #text_change 20-Jun-2000
C; Accession: A33394; Ju0131
R; Ishizaki, J; Ohara, O.; Nakamura, E.; Tamaki, M.; Ono, T.; Kanda, A.; Yoshida, N.;
Biochem. Biophys. Res. Commun. 162, 1030-1036, 1989
A:Title: cDNA cloning and sequence determination of rat membrane-associated phospholi
A:Reference number: A33394; MUID:89350908; PMID:2764915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 AHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM--N 123
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R;Komada, M.; Kudo, I.; Mizushima, H.; Kitamura, N.; Inoue, K.
J. Biochem. 106, 545-547, 1389
A)Title: Structure of cDNA coding for rat platelet phospholipase A2.
A;Reference number: JU0131; MUID:90110043; PMID:2606907
                                                                                                                                                                                                                                                                                                                                  DB 2; Length 146;
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-hoa 56; Indels
                                                                                                                      A.Molecule type: protein
A.Residues: 22-29, 'X', 31-32, 'X', 34 <AAR>
A.Residues: 22-29, 'X', 31-32, 'X', 34 <AAR>
C.Superfamily: phospholipase A.2
C.Keywords: carboxylic ester hydrolase; lipid degradation
F:68,113/Active site: His, Asp #status predicted
                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                       ch 30.8%; Score 294.5; I
l Similarity 42.3%; Pred. No. 3.5e-
60; Conservative 20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 KSYSLKYQFYPNKFCKGKTPSC 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-146 <KOM>
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A; Molecule type: mRNA
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C;Species: Cavia porcellus (guinea pig)
C;Species: Cavia porcellus (guinea pig)
C;Species: Cavia porcellus (guinea pig)
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 18-Jun-1999
C;Accession: 148093
R;Vial, D.; Senorale-Pose, M.; Havet, N.; Molio, L.; Vargaftig, B.B.; Touqui, L.
J. Biol. Chem. 270, 17327-17332, 1995
A;Title: Expression of the type-II phospholipase A2 in alveolar macrophages. Down-regula
A;Reference number: 148093; MUID:9534052; PMID:7615534
A;Reference number: 148093
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Mosidues: 1-145 <RES>
A;Cross-references: EMBL:X82631; NID:9951010; PIDN:CAA57953.1; PID:9951011
C;Superfamily: phospholipase A2
C;Keywords: Carboxylic ester hydrolase
F;67,112/Active alte: His, Asp #status predicted
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A;Cross-references: EMBL:X51529; NID:956930; PIDN:CAA35909.1; PID:956931
R;Aarsman, A.J.; Schalkwijk, C.G.; Neys, F.W.; Iijima, N.; Wherrett, J.R.; van den Bosch
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C:Species: Rattus norvegicus (Norway rat)
C:Deccies: Rattus norvegicus (Norway rat)
C:Datte: 14-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 18-Jun-1999
C:Accession: A35493; S:1388; S71310
R:Komada, M.; Kudo, I.; Inoue, K.
Biochem. Biophys. Res. Commun. 168, 1059-1065, 1990
A;Title: Structure of gene coding for rat group II phospholipase A-2.
A;Reference number: A35493
A;Status: preliminary
                                                82 YVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLMN--QTYREEYRGFLNVYCQ 139
                                                                                      60 KWSYYTYSLENG-DIVCG--GDPYCTKVKCECDKRAAICFRDNLKTYKNRYMTFPDIFCT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DRCCVRHDCCYDRLMKRGCGTKFLNYRFT-HKGSSITCS-VRQNSCQKQLCECDKAAAYC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
2 LLQFRKMIKKMIGKEPIVSYAFYGCYCGKGGRGKPKDATDRCCFVHDCCYEKV--TGCDP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-146 <a href="Year">Year</a> (ACOM>
A; Cross-references: GB:M37127; NID:9204318; PIDN:AAA41223.1; PID:9204319
A; Note: the authors translated the codon TAT for residue 42 as Thr
A; Note: the authors translated the codon TAT for residue 42 as Thr
Biochim. Biophys. Acta 1087, 95-97, 1990
A; TILLE: Structure of genomic DNA for rat platelet phospholipase A(2).
A; Reference number: S11388; MuID:90381322; PMID:2400792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 297; DB 2; Length 145; Pred. No. 2.1e-18;
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31.0%; Score 29/; ub
Best Local Similarity 37.4%; Pred. No. 2.1e-
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                                                                                                                                                              140 GPTPNC 145
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55; Conservative
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A; Residues: 1-137 <DEA>
A; Molecule type: mRNA
A; Residues: 1-138 <TSA>
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S68429
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                                                                                                           phospholipase A2 (EC 3.1.1.4), secretory group II - mouse phospholipase A2 (EC 3.1.1.4), secretory group II - mouse c; species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C; Accession: 148342; PC2009; S35948; 149352
R; Mulherkar, R.; Rao, R.S.; Waqle, A.S.; Patki, V.; Deo, M.G.
R; Mulherkar, R.; Rao, R.S.; Wuld: 94029955; PMID: 8267767
A; Reference number: 148342; MulD: 94029955; PMID: 8267767
A; Reference number: 148342
A; Reference number: 148342
A; Reference number: 148342
A; Molecule type: mRNA

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A;Title: A natural disruption of the secretory group II phospholipase A2 gene in inbred A;Reference number: 149352; MuID:95403435; PMID:7673223
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C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 07-May-1999
C;Accession: 559522
R;Tsai, I.H.; Lu, P.J; Wang, Y.M.; Ho, C.L.; Liaw, L.L.
Biochem. J. 311, 895-900, 1995
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A; Residues: 1-18,'V',20-85,'K',87-146 <KEN>
A; Cross-references: EMBL:U32358; NID:9984836; PIDN:AAC52252.1; PID:9984837
C; Superfamily: phospholipase A2
C; Keywords: carboxylic ester hydrolase
F; 68,113/Active site: His, Asp #status predicted
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A; Residues: 22-146 <MUL2>
A; Note: correction of 535948
F; Mulherkar, R.; Rao, R.; Wagle, A.; Patki, V.; Deo, M.
submitted to the EMBL Data Library, July 1993
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A;Residues: 22-115,'R',118-146 <MUL3>
A;Cross-references: EMBL:X74266
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A; Title: Amino acid sequence of a basic Agkistrodon halys blomhoffii phospholipase A2 A; Reference number: A00766; MUID:87000546; PMID:3530322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myotoxin precursor - southern copperhead
C; Species: Agkistrodon contortrix contortrix (southern copperhead)
C; Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C; Accession: S68429; S74296
R; Ac Araujo, H.S.S.; White, S.P.; Ownby, C.L.
Arch. Biochem. Biophys. 326, 21-30, 1996
A; Title: CDNA cloning and sequence analysis of a lysine-49 phospholipase A(2) myotoxi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
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N.Alternate names: phosphatidylcholine 2-acylhydrolase
C;Species: Agkistrodon blomhoffi (mamushi)
C;Date: 17-Mar-1997 *sequence_revision 17-Mar-1987 *text_change 26-Feb-1999
C;Accession: A00766; S43474
R;Forst, S.; Weiss, J.; Blackburn, P.; Frangione, B.; Goni, F.; Elsbach, P. Biochemistry 25, 4309-4314, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL:U21335; NID:g809484; PIDN:AAC59887.1; PID:g809485
A; Accession: S74296
                                                                                                                                                                                                                                                                                                                                                                               61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
29.2%; Score 279.5; DB 2; Length 137;
Best Local Similarity 39.9%; Pred. No. 6.3e-17;
Matches 57; Conservative 23; Mismatches 52; Indels 11;
                                                                                                                                         29.3%; Score 280.5; DB 2; Length 138; 37.4%; Pred. No. 5.2e-17;
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Superfamily: phospholipase A2 F;1-16/Domain: signal sequence #status predicted <SIG>F;1-17/Product: myotoxin #status experimental <MAT>
                                                                                                                                                                                                             52;
A;cross-references: EMBL:X77645
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase
F;63,105/Active site: His, Asp #status predicted
                                                                                                                                                                                                                29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 LMN--QTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 LMN--QTYREEYRGFLNVYCQGP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 LRENLDTYNKKYKAYFKFKCKKP 134
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C; Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Date: 10 *Feb-1995 #sequence_revision 10 *Feb-1995 #text_change 18-Jun-1999
C; Accession: A4999, S.J.; Seilhamer, J.J.; Tischfield, J.A.
J. Biol. Chem. 269, 2365-2368, 1994
A; Title: Cloning and recombinant expression of a novel human low molecular weight Ca(A; Reference number: A49959; MUID: 94131989; PMID: 8300559
                                                                                                                                                                   phospholipase A2 (EC 3.1.1.4) precursor (version 2) - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 24-Jul-1997
C.Accession: JU0283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 AHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM--N 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 THGCCYNLLERRGCGTKFLTYKFSYRGG-QISCS-TNQDSCRKQLCQCDKAAAECFARNK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 VAILA-GSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCCH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Cross-references: GB:103090; NID:9460914; PIDN:AAC28886.1; PID:9460915 C; Superfamily: phospholipase A2 C; Keywords: carboxylic ester hydrolase F; 67,111/Active site: His, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phospholipase A2 (EC 3.1.1.4) low molecular weight, precursor - human
                                                                                                                                                                                                                                                                      R; Komada, M.; Kudo, I.; Mizushima, H.; Kitamura, N.; Inoue, K. J. Biochem. 106, 545-547, 1989
A; Title: Structure of cDNA coding for rat platelet phospholipase A2. A; Reference number: JU0131; MUID: 90110043; PMID: 2606907
A; Accession: JU0283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Keywords: carboxylic ester hydrolase F:1-21/Domain: signal sequence #status predicted <SIG>F:22-146/Product: phospholipase A2 #status predicted <MAT>F:68,113/Active site: His, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sest Local Similarity 40.8%; Pred. No. 1e-1/
Matches 58; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.0%; Score 277.5;
                         125 KSYSLKYQFYPNKFCKGKTPSC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 OTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LMN--QTYREEYRGFLNVYC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: phospholipase A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53; Conservative
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A; Residues: 1-146 <KOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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A; Residues: 1-138 <CHE>
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                                                                                                                          RESULT 12
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                                                                                                                                                                                                       A Molecule type: protein
A Residues: 1-19;50-56 <puv.
A Residues: 1-19;50-56 <puv.
C; Complex: homodimer
C; Complex: homodimer
C; Function:
A Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-A; Note: the reaction is strongly enhanced when the phospholipid is condensed into a mice C; Superfamily: phospholipase A2
C; Reywords: calcium: carboxylic ester hydrolase; homodimer; lipid degradation; metallopr F; 26-115,28-44,43-95,50-88,57-81,75-86/Disulfide bonds: #status predicted
F; 27,29,31,48/Binding site: calcium (Tyr, Gly, Gly, Asp) #status predicted
F; 47,89/Active site: His, Asp #status predicted
F; 49-112/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G:Species: Bothrops jararacussu (jararacussu)

G:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999

G:Accession: ISO098; 844247

G:Accession: ISO098; A4247

J: Mol. Evol. 41, 174-179, 1995

A:Title: The molecular cloning of a phospholipase A2 from Bothrops jararacussu snake ver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ;
                                                                                                               Eur. J. Biochem. 221, 481-490, 1994
Affilte: Inhibition of human secretory class II phospholipase A(2) by heparin.
Affecence number: 843474; MUID:94222096; PMID:8168536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Molecule, type: mRNA
A;Residues: 1-138 <MOU>
A;Cross-references: EMBL:X76289; NID:g475923; PIDN:CAA53921.1; PID:g475924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 LINLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDMCCHAHDCCYQELFDQGCHP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.1%; Score 278.5; DB 1; Length 122; 37.3%; Pred. No. 6.9e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 138;
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A:Status: preliminary: translated from GB/EMBL/DDBJ
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37.4%; Pred. No. 7.8e-17;
tive 21; Mismatches 60
                    A;Molecule type: protein
A;Residues: 1-122 <POR>
A;Note: the identification of 74-Val is tentative
R;Dua, R.; Cho, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 37.3%; Pred. No. v.sc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Gene: PLA-2
C;Superfamily: phospholipase A2
F;63,105/Active site: His, Asp #status predicted
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A: Accession: A00766
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Search completed: February 10, 2003, 10:37:54 Job time : 18 secs
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A.Residues: 'Z',89-118 <AIR2>
C;Comment: This subunit has no enzymatic or toxin activity. It helps target crotoxin bas
C;Complex: heterodimer of acidic and basic subunits; mature acidic subunit has 3 chains,
C;Complex: heterodimer of acidic and basic subunits; mature acidic subunit has 3 chains,
C;Superfamily: phospholipase A2
C;Reywords: calcium; heterodimer; metalloprotein; pyroglutamic acid; venom
F;1-16/Domain: signal sequence #status predicted <SIG>
F;1-36/Domain: propeptide #status predicted <PRO>
F;39-76,84-118,125-138/Product: crotoxin acidic subunit #status experimental <MAT>
E;39-76/Domain: crotoxin acidic subunit chain A #status experimental <CHA>
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                                                                                                                                                                                                                                                                                                    R;Chen, J.; Engle, S.J.; Seilhamer, J.J.; Tischfield, J.A.
R;Chen, J.; Engle, S.J.; Seilhamer, J.J.; Tischfield, J.A.
J. Biol. Chem. 269, 23018-23018-23024, 1994
A;Title: Cloning and characterization of novel rat and mouse low molecular weight Ca(2+)
A;Reference number: A54762; MUID:94364995; PMID:8083202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phospholipase A2 homolog crotoxin acidic subunit precursor - tropical rattlesnake phospholipase A2 homolog crotoxin acidic subunit precursor - tropical rattlesnake, cascabel) c; Species: Crotalus durissus terrificus (tropical rattlesnake, cascabel) c; Species: 30-Sep-1991 #text_change 11-Jun-1999 C; Accession: S01392; A23861; S11382; B23861; C23861 Revolhier, C.; Ducancel, F.; Guignery-Frelat, G.; Bon, C.; Boulain, J.C.; Menez, A. Nucleic Acids Res. 16, 9050, 1988 A. Title: Cloning and sequencing of cDNAs encoding the two subunits of crotoxin. A. Reference number: S01392; MUID:89016587; PMID:3174444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PILNAYQFTIVNGTVFCGCTVASSCPCGQKACECDKQSVYCFKENLATYEKAFKQLF--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 PYVDHYDHTIENNTEIV-CSDLNKTECDKQTCMCDKNWVLCLMNQ--TYREEYRGFLNVY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 SLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCCHAHDCCYQELFDQGCH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | SFWQFQRWVKHVTGRSAFFSYYGXGCYCGLGGKGLPVDATDRCCWAHDCCYHKLKEWGCQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X12606; NID:g62685; PIDN:CAA31126.1; PID:g62686 R;Aird, S.D.; Kaiser, I.I.; Lewis, R.V.; Kruggel, W.G. Biochemistry 24, 7054-7058, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50; Indels
                                                                                                                                                                                                                                                                                      J.J.; Tischfield, J.A.
                                                                                                                                                          phospholipase A2 (EC 3.1.1.4) MPL2-8 - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 7%; Score 275; DB 2;
ilarity 41.9%; Pred. No. 1.5e-16;
Conservative 15; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase
118 LKRNLRSYNPQYQYFPNILC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-138 <BOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 CQGPT-PNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 ---PTRPQC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-130 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A23861
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                                                                                                                                                                                                                                                                    C; Accession: A54762
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A54762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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F;125-138/Domain: crotoxin acidic subunit chain C #status experimental <CHC>F;125-131,44-60,59-111,65-138,66-104,73-97,91-102/Disulfide bonds: #status predicted F;43-45,47,64/Binding site: calcium (Tyr. Gly. Asp) #status predicted F;84/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experi F;125/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status exper
F;84-118/Domain: crotoxin acidic subunit chain B #status experimental <CHB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 DRCCFEHDCCYAKL--TGCDPTTDVYTYRQEDG-EIVCGE--DDPCGTQICECDKAAAIC 111
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                       1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                              28.5%; Score 272.5; DB 1; Length 138; 39.5%; Pred. No. 2.5e-16;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                        Score ......
pred. No. 2.5e-16;
                                                                                                                                                                                                                                                                                      18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LMN--QTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 FRNSMDTYDYKYLQFSPENCQGESQPC 138
                                                                                                                                                                                                                                                               Best Local Similarity 39.53
Matches 58; Conservative
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 10, 2003, 10:35:27 ; Search time 12 Seconds (without alignments) 580.669 Million cell updates/sec Run on:

1 MKKFFTVAILAGSVLSTAHG........EPPPEEVTCSHQSPAPPAPP 168 US-09-975-456B-2 957 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			u snu	OHOU!		trim		OIIIOU		trimer	_	ratt	Obdex a musculu		O9qzt3 rattus norv	P31482 mus musculu			agkistrod		homo sapi				tr1me	P48650 echis carin		vipera		vipera		P04361 agkistrodon	Q9i834 bothrops mo	agkistroc
SUMMARIES		1 PAZF HUMAN	PAZE	PA2D				PAZE			DA2M	PAZA					1 DAJE MOUSE					1 PA2A CBORT								PAZA			PAZH_AGKPI	FAZZ	L PAZI_AGKPI
	Length [168	168	145	144	138	142	142	144	122	145	146	151	150	151	146	137	137	122	138	3.5												121		
æ	Query	٠.	78.1	٠.		- 1		32.3	-		31.0				29.5		29.3	29.2	29.1	29.1	28.8	28.5	28.5	28.4	28.4	28.2	28.1	28.1	28.1	28.0	0.40	, , ,	27.0		? •
	Score	957	747	353	344.5	319.5	313.5	309	302.5	298.5	297	287.5	283.5	282	282	281	280.5	279.5	278.5	278.5	275.5	272.5	272.5	272	272	269.5	268.5	268.5	268.5	267.5	267	264 5	262	261 5) ;
	Result No.	-	7	m	4	ß	9	7	æ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	<u>-</u>	35	33	}

P14424 vipera ammo P20249 agk istrodon P20474 bothrops as P20471 trimeresuru P24605 bothrops as P82287 bothrops pl P20476 trimeresuru P58399 bothrops pl P07517 crotalus du Q90249 bothrops ja P31854 vipera beru Q98996 vipera pala
PA2B_VIPAA PA22_AGKHA PA21_BGTAS PA22_BGTAS PA22_BGTPI PA32_BGTPI PA31_BGTPI PA3B_CRODU PA3H_BGTJR PA2H_BGTJR PA2H_BGTJR
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138 122 132 138 121 121 138 122 138
W440008748441
27.3 27.1 27.1 27.1 27.1 26.9 26.3 26.3 26.2 26.2 26.2
261.5 260 260 260 260 250.5 255.5 255.5 250.5 260.5
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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. Hydrolyzes phosphatidylglycerol versus phosphatidylglycerol versus phosphatidylcholine with a 15-fold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last amontation update)
15-JUN-2002 (Rel. 41, Last amontation update)
15-JUN-2002 (Rel. 41, Last amontation (EC 3.1.1.4)
Group IIs secretory phospholipase A2 precursor (EC 3.1.1.4)
(phosphatidylcholine 2-acylhydrolase GIIF) (GIIF spLA2) (spLA(2)-IIF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DWCCHAHDCCYQELFDQGCHPYVDHYTENNTEIVCSDLNKTECDKQTCMCDKNWVLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDILINE-20002639; PubMed=10531313; MEDILINE-20002639; PubMed=10531313; Machanin E., Ghomashchi F., Gelb M.H., Lazdunski M., Lambeau G.; "On the diversity of secreted phospholipases A2. Cloning, tissue distribution, and functional expression of two novel mouse group II
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                   BY SIMILARITY.
N-LINKED (GLCNAC. ...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
             POTÉNTIAL.
GROUP IIF SECRETORY PHOSPHOLIPASE A2
                                                                                                                                                                                                                                                                                                                                                                                                      Score 957; DB 1; Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preference. (By similarity).
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
acylqlycerophosphocholine + a fatty acid anion.
-!- COFACTOR: Binds 1 calcium ion per subunit.
-!- SUBCELLUAR LOCATION: Secreted.
-!- SUBLERITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LMNQTYREEYRGFLNVYCQGPTPNCSIYEPPPEEVTCSHQSPAPPAPP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                  35B159298246A762 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     pred. No. 4.1e-79;
0; Mismatches 0;
degradation; Signal; Calcium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 AA.
                                                  BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                          168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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Q9QZT4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  168;
       Hydrolase;
                                                          ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                 DISULFID
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                         SIGNAL
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Group IID secretory phospholipase A2 precursor (EC 3.1.1.4)
Group IID secretory phospholipase A2 precursor (EC 3.1.1.4)
(SPLA(2)-IID) (Secretory-type PLA, stroma-associated homolog).
PLAAGGED OR SPLASH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
VIA CARBONYL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. GECRETORY PHOSPHOLIPASE A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9E15FB6AC0F5450C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.1%; Score 747; DB 1; 75.2%; Pred. No. 2.8e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Lipid degradation; Signal; Calcium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
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                                                                                                                                                                                          HSSP; p00593; 4BP2.
MGD: MGI:1349661; pla292f.
InterPro: IPR001211; phospholipaseA2.
Pfam; PF00068; phoslip; 1.
                                                                                                                                                                                                                                                                                                                                         SMART; SM00085; PA2C; 1.
PROSITE; PS00119; PA2_ASP; FALSE_NEG.
PROSITE; PS00118; PA2_HIS; 1.
                                                                                                                                                                                                                                                                                         PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 V
51 V
68 B
1880 MW;
                                                                                                                                                                   EMBL; AF166099; AAF04500.2; -.
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1114
1138
164
1120
1113
1106
1111
144
47
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Matches 124;
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SEQUENCE
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                                                                                                                                                                                                                "SPIASH (PLA(2)11D), a novel member of phospholipase A2 family, is associated with lymphotoxin-deficiency."; Genes Immun. 1:191-199(2000).
Kawamoto K., Fujii N., Arita H., Hanasaki K.;
"Cloning and characterization of novel mouse and human secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
GROUP IID SECRETORY PHOSPHOLIPASE A2.
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( BY SIMILARITY).
( BY SIMILARITY).
( BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Calcium; Polymorphism.
                                                   SEQUENCE FROM N.A.
MEDLINE-21040292; PubMed-11196711;
Shakhov A.N., Rubtsov A.V., Lyakhov I.G., Tumanov A.V.,
                                                                                                                                                              Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARÎTY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIA CARBONYL OXYGEN
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                               Biol. Chem. 274:24973-24979(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00068; phosiip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
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EMBL; AF188625; AAF09020.1; -
EMBL; AL158172; CAC13159.1; -
EMBL; BC025706; AAH25706.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SMO0085; PA2C; I.
PROSITE; PS00119; PA2_ASP; I.
PROSITE; PS00118; PA2_HIS; I.
Hydrolase; Lipid degradation;
                                                                                                                                                                                                TISSUE-Pancreas, and Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC: 9033; PLA2G2D.
                       phospholipase A2s.";
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                    SEQUENCE FROM N.A.
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63 CCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNWVLCLM 122
                                                                                                                                                                                                                                            63 CCQTHDCCYDHLKTQGCSIYKDYYRYRYFSQG-NIHCSD-KGSWCEQQLCACDKEVAFCLK 120
                                                                                                                      8; Gaps
                                                                                                                                              7 VAILAGSVLSTA----HGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDW 62
                                                                                                                                                                   :|:| | |:
3 LALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGGPKDATDW 62
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MEDLINE-2108560; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
Arakawa T., Hara A., Putunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "SPLASH (PLA(2)IID), a novel member of phospholipase A2 family, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Group IID secretory phospholipase A2 precursor (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase GIID) (GIID spLA2) (PLA2IID) (Secretory-type PLA, stroma-associated homolog). PLA2G2D OR PLA2A2 OR SPLASH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ishizaki J., Suzuki N., Higashino K.-I., Yokota Y., Ono T., Kawamoto K., Fujii N., Arita H., Hanasaki K.; "Cloning and characterization of novel mouse and human secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lazdunski M., Lambeau G.;
Cloning and recombinant expression of a novel mouse-secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-99315857; PubMed-10383420;
Valentin E., Koduri R.S., Scimeca J.-C., Carle G., Gelb M.H.,
Lazdunski M., Lambeau G.;
                                                                                Length 145;
                                                                                                                      Indels
                   /FTId-VAR_012741.
145 AA; 16546 MW; CF3A49DE516BDIEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21040292; Pubmed-11196711;
Shakhov A.N., Rubtsov A.V., Lyakhov I.G., Tumanov A.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION,
                                                                          Score 353; DB 1;
Pred. No. 5.2e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                          O9WVF6; O9JIKO;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 144 AA.
                                                                                                              19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated with lymphotoxin-deficiency."; Genes Immun. 1:191-199(2000).
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J. Biol. Chem. 274:24973-24979(1999).
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                                                                                                                                                                                                                                                                                            123 N--QTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                           121 RNLDTYOKRLRFYWRPHCRGOTPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99386983; PubMed=10455175;
                                                                        36.98;
                                                                                        Local Similarity 45.5%
les 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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Nedospasov S.A.;
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                                                                        Query Match
VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                               acyl groups in 3-n-phosphoglycerides. L-alpha-1-palmitoyl-2-
acyl groups in 3-n-phosphoglycerides. L-alpha-1-palmitoyl-2-
linolecyl phosphatidylethanolamine is more efficiently hydrolyzed
than the other phospholipids examined.
C-1-CATATATIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
acylglycerophosphocholine + a fatty acid anion.
C-1-COFACTOR: Binds 1 calcium ion per subunit.
C-1-SUBCELLULAR LOCATION: Secreted (isoform 1) and Cytoplasmic
(isoform 2) (Potential).
C-1-ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
produced by a leternative splicing.
C-1-TISSUE SPETIFICITY: Expressed in several tissues including
pancreas, spleen, thymus, skin, lung, and ovary.
C-1-STMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
C-1-STMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninici P., de Bonaldo M.F., Gustincich S., Hill D., Heicher C., Fujita M., Gariboldi M., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00119; PA2_ASP; 1.
PROSITE; PS00118; PA2_HIS; 1.
Hydrolase; Lipid degradation; Signal; Calcium; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
GROUP IID SECRETORY PHOSPHOLIPASE A2.
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VIA CARBONTL OXYGEN (BY SIMILARITY).
VIA CARBONTL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.; "Function of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY.
SSING (IN ISOFORM 2).
7697ADA07F8D270A CRC64;
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ProDom; PD000303; PhospholipaseA2; 1.
SMART; SM00085; PA2c; 1.
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EMBL, AF124374; AAF09019.1;
EMBL, AF166407; AAF42987.1;
EMBL, AF169408; AAF42988.1;
EMBL, AK016005; BAB31033.1;
EMBL, AK01232; BAB33230.1;
HSSP; P24605; 1CLP.
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                                  RRARAR RR
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Query Match

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EMBL; D10721; BAA01564.1; -.
45.18;
                                                         STANDARD;
                                                                                                                                                                                                           16
138
63
105
131
111
138
Best Local Similarity
                                                                                          NCBI_TaxID=88087;
                                                                                                                                                                                                            105
63
105
42
44
59
                                                                                                                                                                             P51972;
                                                         PA2Y_TRIFL
002517;
                                                                                                                                                                                                                              DISULFID
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DISULFID
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                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                         Signal.
                                                                                                                                                                                                            SIGNAL
                                                     Y_TRIFL
   Matches
                                                   RESULT 5
                                                            δŏ
                                                                                                                                                                                                                                   Score 344.5; DB 1; Length 144;
                                                                                                                                                                                                                              16164 MW;
                                                                                                                                                                                                                                    36.0%;
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                                            4
                                                                                                                                                                                                                                                                           63 CQKHDCCYAHLKIDGCKSLTDNYKYSISQGT-IQCSD-NGSWCERQLCACDREVALCLKG 120
                                                                                                                                                                                                                                      64 CHAHDCCYQELFDQCCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMYLCLMN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=92409555; Pubmed=1528861;
Ogawa T., Oda N., Nakashima K.-I., Sasaki H., Hattori M., Sakaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kihara H., Ohno M.;
"Unusually high conservation of untranslated sequences in cDNAs for Trimeresurus flavoviridis phosphollpase A.2 isozymes.";
Proc. Natl. Acad. Sci. U.S.A. 89:8557-851(1992).
-!- FUNCTION: PAZ CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2-ACYL GROUPS IN 3-SN-PHOSPHOGIXCERIDES.
2-ACYL GROUPS IN 3-SN-PHOSPHOGIXCERIDES.
-!- CATALYTIC ACTIVITY: Phosphatidylcholling + H(2)O = 1-
                                                                                                         7 VAILAGSVL---STAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWC 63
                                                                                                                                                 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Lipid degrādation; Calcium; Multigene family; Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acylglycerophosphocholine + a fatty acid anion.
-!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHOLIPASE A2 ISOZYME PL-X'.
Pred. No. 3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OlrEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-70N-2002 (Rel. 41, Last annotation update)
15-phospholipase A2 isozyme PL-X' precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase)
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                                                      65; Conservative 20; Mismatches
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Pfam; PF00068; phosalb; 1.
PRINTS; PR00389; PHPHLIPASEA2.
ProDom; P0000303; PhospholipaseA2; 1.
                                                                                                                                                                                                                                                                                                                                                                                 124 -- QTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NLDSYNKRLRYYWRPRCKGKTPAC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trimeresurus flavoviridis (Habu).
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PROSITE; PS00118; PA2_HIS; 1.
PROSITE; PS00119; PA2_ASP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase GIIE) (GIIE SPLA2) (SPLA(2)-IIE).
                                                                                                                                                                                                                                                                                                                                                                                                                61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                  1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                                                                                                                                                               Suzuki N., Ishizaki J., Yokota Y., Higashino K., Ono T., Ikeda M., Fujil N., Kawamoto K., Hanasaki K.; "Structures, enzymatic properties, and expression of novel human and J. Biol. Chem. 275:5785-5793(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEQUENCE FROM N.A.
MEDLINE-20002639; PubMed-10531313;
MEDLINE-20002639; PubMed-105313;
MEDLINE-20002639; PubMed-10531313;
MEDLINE-20002639; PubMed-105313;
MEDLINE-2000263
                                                                           VIA CARBONYL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                  DB 1; Length 138;
                                                                                                                                                    BY SIMILARITY.
471B01878CCA1ED1 CRC64;
                                                                                                                                                                                                                                                                                49;
                                                                                                                                                                                                                                                    5e-22;
       BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                           28; Mismatches
                                                                                                                                                                                                                               Score 319.5;
Pred. No. 5e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LMN--OTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 FRDNLKTYKKRYMTFPDIFCTDPTEKC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 274:31195-31202(1999).
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                                                                                                                                                                        15733 MW;
                                                                                                                                                                                                                                                 40.18;
                                                                                                                                                                                                                                                                   59; Conservative
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47
64
138 AA;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)

[Phosphatidylcholine 2-acylhydrolase GIIE) (GIIE SPLA2) (sPLA2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 DWCCHAHDCCYGRLEKLGCDPKLEXYLFSITRD-NIFCA--GRTACQRHTCECDKRAALC 115
                                                                                                                                                                                              BY SIMILARITY
VIA CARBONYL OXYGEN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                          7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
GROUP IIE SECRETORY PHOSPHOLIPASE A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 142;
                                                                                                                                                                                                                                                                                                                                                           32.8%; Score 313.5; DB 1; Length 1
.ilarity 42.2%; Pred. No. 1.8e-21;
Conservative 20; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                         8B0E3CC710A1F946 CRC64;
                                                                                                               SMART; SM00085; PA2C; 1.
PROSITE; PS00119; PA2_ASP; FALSE_NEG.
PROSITE; PS00118; PA2_HIS; 1.
Hydrolase; Lipid degradation; Signal; Calcium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 142 AA.
                                                                                                                                                                                        BY SIMILARITY
                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
or send an email to license@isb-sib.ch).
                                                      MGD; MGI:1339660; Pla2g2e.
InterPro; IPR001211; PhospholipaseA2.
PFf00068; Phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 LMN--QTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 FRHNLNTYNRKYAHYPNKLCTGPTPPC 142
                       EMBL; AF166098; AAF04499.1; -. EMBL; AF112984; AAF22290.1; -.
                                                                                                                                                                                                                                                                                                                                      15942 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                      142 AA;
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65
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                                                HSSP; P14555;
                                                                                                                                                                                                                                                                                                                                                                                 62;
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Q9NZK7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 HPYVDHYDHIIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLMNQ--TYREEYRGFLNVY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 EPKLEKYLFSV-SERGIFCA--GRTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIAL HUMAN STANDARD; PRT; 144 AA. p14555; 09UCD2; 01-70002; 13, Created) 01-3NN-1990 (Rel. 14, Last sequence update) 15-JUN-2002 (Rel. 14, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) phospholipase A2, membrane associated precursor (EC 3.1.1.4) (Phospholipase A2, membrane associated precursor (EC 3.1.1.4) (Phospholipase A2) (GIIC sPLA2) (Non-panorealic secretory phospholipase A2) (NPS-PLA2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 GSLLNLKAMVEAVTGRSAILSFVGYGGYCGLGGRGQPKDEVDWCCHAHDCCYQELFDQGC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
VIA CARBONYL OXYGEN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
WM; 3C360EA710E141FB CRC64;
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                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
GROUP IIE SECRETORY PHOSPHOLIPASE A2.
BY SIMILARITY.
                acylglycerophosphocholine + a fatty acid anion.
-- COFACTOR: Binds I calcium ion per subunit.
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Restricted to the brain, heart, lung, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 309; DB 1; Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
                                                                          placenta.
-1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
                                                                                                                                                                                                                                                                                                           PROSITE; PSOU119; PA2_ASP; FALSE_NEG. PROSITE; PSOU118; PA2_HIS; 1. Hydrolase; Lipid degradation; Signal; Calcium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Mismatches
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InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phostir.
                                                                                                                                                                                                                                                              pfam: PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15989 MW;
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                                                                                                                                                                                                                                                                                                     SM00085; PA2c;
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142 AA;
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SEQUENCE OF 21-54.

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MEDLINE-89197814; Pubmed=3240982;
Hara S., Kudo I., Matsuta K., Miyamoto T., Inoue K.;
Hara S., Kudo I., Matsuta K., Miyamoto T., Inoue K.;
"Amino acid composition and NH2-terminal amino acid sequence of human phospholipase A2 purified from rheumatoid synovial fluid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The primary structure of a membrane-associated phospholipase A2 from human spleen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kramer R.M., Johansen B., Hession C., Pepinsky R.B.; "Structure and properties of a secretable phospholipase A2 from human niatelete".
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WEDLINE-91287826; PubMed=2062381;
Wery J.-P., Schevitz R.W., Clawson D.K., Bobbitt J.L., Dow E.R.,
Gamboa G., Goodson T. Jr., Hermann R.B., Kramer R.M., McClure D.B.,
Mihelich E.D., Putnam J.E., Sharp J.D., Stark D.H., Teater C.,
Warrick M.W., Jones N.D.;
"Structure of recombinant human rheumatoid arthritic synovial fluid
"Structures of recombinant human rheumatoid arthritic synovial Mature 352:79-82(1991).
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89174633; PubMed=2925633;
Kramer R.W., Hession C., Johansen B., Hayes G., McGray P., Chow E.P.,
Tizard R., Pepinsky R.B.;
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MEDLINE-94002200; PubMed-8399335;
Minami T., Tojo H., Shinomura Y., Matsuzawa Y., Okamoto M.;
Minami T., Tojo H., Shinomura Y., matsuzawa P., Okamoto M.;
                                                                                                                                                                                                                                         "Cloning and recombinant expression of phospholipase A2 present in rheumatoid archritic synovial fluid."; J. Biol. Chem. 264:5335-5338(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure and properties of a human non-pancreatic phospholipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Synovial fluid;
MEDLINE-89076274; PubMed=3202859;
Lai C.Y., Wada K.;
Phospholipase A2 from human synovial fluid: purification and structural homology to the placental enzyme.";
Piochem. Biophys. Res. Commun. 157:488-493(1988).
                                                                                                                                                                                     Seilhamer J.J., Pruzanski W., Vadas P., Plant S., Miller J.A.,
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kanda A., Ono T., Yoshida N., Tojo H., Okamoto M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 163:42-48(1989).
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                                                                                                         SEQUENCE FROM N.A.
TISSUE=Rheumatoid arthritic synovial fluid;
MEDLINE=89174566; PubMed=2925608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exp. Med. Biol. 275:35-53(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 264:5768-5775(1989).
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                                                 NCBI_TaxID=9606;
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**RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).

**REDLINE=99207049; PubMed=9538252;

**RITAGOKOTO K., Hagishira S., Sato T., Ohtan M., Miki K.;

**KITAGOKOTO K., Hagishira S., Sato T., Ohtan M., Miki K.;

**Crystal structure of human secretory phospholipase A2-IIA complex

**TOTYSTAL STATE STATE STATE STATE STATE STATE STATE STATE

**TOTYTON: THOUGHT TO PARTICIPATE IN THE REGULATION OF THE PHOSPHOLIPID METABOLISM IN BIOMEMBRANES INCUDING EICOSANOID

**ROYNTHESIS: CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2-

**ACL GROUPS IN 3-SN-PHOSPHOCIYCENDES.**

**CATALYTIC ACTYVITY: Phosphatidylcholine + H(2)O = 1-

**ACL GROUPS IN 3-SN-PHOSPHOCIYCENDES.**

**COFACTOR: Binds I calcium ion per submit.**

**COFACTOR: Binds I calcium ion per submit.**

**INSCELLULAR LOCATION: Membrane-associated.**

**AND ALSO EXTRACELULARLY: THE MEMBRANE-BOUND AND SECRETED FORMS CHES ARE IDENTICAL AND ARE ENCODED BY A SINGLE GENE.**

**ARE IDENTICAL AND ARE ENCODED BY A SINGLE GENE.**

**COFACTOR: SMILLARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                  MEDLINE-9539325; PubMed-5664108; Schevitz R.W., Bach N.J., Carlson D.G., Chirgadze N.Y., Clawson D.K., Schevitz R.W., Bach N.J., Carlson D.G., Chirgadze N.Y., Clawson D.K., Olilard R.D., Draheim S.E., Hartley L.W., Jones N.D., Mihelich E.D., Structure-based design of the first potent and selective inhibitor of human non-pancreatic secretory phospholipase A2.";
                                                                                 Structures of free and inhibited human secretory phospholipase A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED.
                                 MEDLINE-92054586; Pubmed-1948070;
Scott D.L., White S.P., Browning J.L., Rosa J.J., Gelb M.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Lipid degradation; Membrane; Signal; Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
                X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
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PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M22430; AAA36550.1; --
EMBL; M22431; AAA36549.1; --
EMBL; BC005919; AAH05919.1; --
PIR; A32862; PSHUYE.
                                                                                                    from inflammatory exudate."; Science 254:1007-1010(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00085; PA2c; i.
PROSITE; PS00118; PA2_HIS; 1.
PROSITE; PS00119; PA2_ASP; 1.
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67
111
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LBBC; 31-OCT-93.
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1DB5; 12-NOV-99
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                                                                    Sigler P.B.;
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61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
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                                                                                                                                                                                                                                                                                                                5; Gaps
                                                                                                                                                                                                                                                                                                                            1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPRDEV 60
                                                                                                                                                                                                                                                                                                                                         Mini R.M., Kawabata S.-I., Iwanaga S., Comparison of amino terminal region of three isoenzymes of from parison of amino terminal region of three isoenzymes of flavoviridis (habu snake) venom and the complete amino acid sequence of the basic phospholipase, TFV PL-X.";

Toxicon 24:1117:1129[1986].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- FUNCTION: PAZ CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
-1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase A2 isozyme PL-X (EC 3.1.1.4) (Phosphatidylcholine 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                           Length 144;
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                    16083 MW; 923C5FA0C6979CDA CRC64;
                                                                      VIA CARBONYL OXYGEN.
VIA CARBONYL OXYGEN.
VIA CARBONYL OXYGEN.
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                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                     31.6%; Score 302.5; DB 1
ilarity 38.8%; Pred. No. 1.7e-20;
Conservative 24; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 AA.
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MEDLINE=87179112; PubMed=3564060;
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  144 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 KWSYYTYSLENG-DIVCG--GDPYCTKVKCECDKRAAICFRDNLKTYKNRYMTFPDIFCT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Expression of the type-II phospholipase A2 in alveolar macrophages. Down regulation by an inflammatory signal.";
J. Biol. Chem. 270:17327-17332(1995)
-!- FUNCTION: THOGRATT OP PARTICIPATE IN THE REGULATION OF THE PHOSPHOLIPID METABOLISM IN BIOMEMBRANES INCLUDING EICOSANOID BIOSYNTHESIS (BY SIMILARITY). CATALXZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                 7; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia
                                                                                                                                                                                                                                                                           VIA CARBONYL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
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STRAIN-Hartley; TISSUE-Macrophage;
MEDLINE-95340522; PubMed-7615534;
Vial D., Senorale-Pose M., Havet N., Molio L., Vargaftig B.B.,
                                                                                                                           PROSITE; PSO0118; PA2_HIS; 1.
PROSITE; PS00119; PA2_ASP; FALSE_NEG.
Hydrolase; Lipid degradation; Calcium; Multigene family; Venom.
   -i- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
                                                                                                                                                                                                                                                                                                                                                    Score 298.5; DB 1; Length 122; Pred. No. 3.3e-20;
                                                                                                                                                                                                                                                                                                                                                                            23; Mismatches 44; Indels
                 -- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
A9D652276C5D0DF0 CRC64;
                                                                                                                                                                BY SIMILARITY
                                                                                                      ProDom; PD000303; PhospholipaseA2; 1. SMART; SM00085; PA2c; 1.
                                                               Interpro: IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
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(Rel. 33, Last sequ
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44
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88
                                            PIR; A25500; PSTVXF.
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                                                           HSSP; P51972; 1VAP
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PLA2G2A.
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-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
acylglycerophosphocholine + a fatty acid anion.
-!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Membrane-associated.
-!- TISSUE SPECIFICITY: ALVEDLAR MACROPHAGES, AND AT MUCH LOWER LEVELS
-!- IN PERIPHERAL BLOOD MONOCYTES AND PERITONEAL MACROPHAGES.
-!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE AZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DRCCVRHDCCYDRLMKRGCGTKFLNYRFT-HKGSSITCS-VKQNSCQKQLCECDKAAAYC 118
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15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIA CARBONYL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Lipid degradation; Membrane; Signal; Calcium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
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Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
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PROSITE; PS00118; PA2_HIS; 1.
PROSITE; PS00119; PA2_ASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X82631; CAA57953.1; -. HSSP; P14555; 1POD.
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PLA2G2A.
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P14423;
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DISULFID
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A ABLEBMAN A.3., de Jong J.G.N., Arnoldussen E., Neys F.W.,
A ABLEBMAN A.3., de Jong J.G.N., Arnoldussen E., Neys F.W.,
A van Wassenaar P.D., van den Bosch H.;
Immunoaffaltatjon of rat liver phospholipase A2.";
J. Biol. Chem. 264:10008-10014 (1989).
-!- FUNCTION: THOUGHT TO PARTICIPATE IN THE REGULATION OF THE PHOSPHOLIPID METABOLISM IN BIOMEMBRANES INCLUDING EICOSANOID
BIOSYNTHESIS. CAPALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2-
ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CATALYTIC ACTIVITY: Phosphatidylcholine + Gatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- MISCELLUAR LOCATION: Membrane-associated.
CC -!- MISCELLANEOUS: GROUP II PHOSPHOLIPASE A2 IS FOUND IN MANY CELLS
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

BEDLINE-89350908; PubMed-2764915;
Ishlzaki J., Ohara O., Nakamura E., Tamaki M., Ono T., Kanda A., Yoshida N., Teraoka H., Tojo H., Okamoto M.;
"CDNA cloning and sequence determination of rat membrane-associated phospholipase A2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayakawa M., Horigome K., Kudo I., Tomita M., Nojima S., Inoue K.; "Amino acid composition and NH2-terminal amino acid sequence of rat platelet secretory phospholipase A2."; J. Biochem. 101:1311-1314(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ono T., Tojo H., Kuramitsu S., Kagamiyama H., Okamoto M.; Purification and characterization of a membrane-associated phospholipase A2 from rat spleen. Its comparison with a cytosolic phospholipase A2 S-1.";
                                                                      STRAIN-Sprague-Dawley; TISSUB-Platelet;
MEDLINE-99110043; PubMed-2606907;
Komada M., Kudo I., Mizushima H., Kitamura N., Inoue K.;
"Structure of cDNA coding for rat platelet phospholipase A2.";
"). Blochem. 106:545-547(1989).
                                                                                                                                                                                                                                         Komada M., Kudo I., Inoue K.;
"Structure of gene coding for rat group II phospholipase A2.";
Blochem. Blophys. Res. Commun. 168:1059-1065(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Sprague Dawley, TISSUB-Liver;
MEDINE-99181122; PubMed-2400792;
Kusunoki C., Satoh S., Kobayashi M., Niwa M.;
"Structure of genomic DNA for rat platelet phospholipase A2.";
Blochim. Blophys. Acta 1087:95-97(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Wistar; TISSUE-Platelet;
BEDIARE-89174508; Pubmed-2235451;
Hayakawa M., Kudo I., Tomita M., Nojima S., Inoue K.;
"The primary structure of rat platelet phospholipase A2.";
J. Blochem. 104:767-772(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                              Blochem. Blophys. Res. Commun. 162:1030-1036(1989).
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                                                                                                                                                                                                                       MEDLINE-90267443; PubMed-2346480;
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MEDLINE-89255484; Pubmed-2722857;
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                    SEÓUENCE FROM N.A.
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                     NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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 AND ALSO EXTRACELLULARLY. THE MEMBRANE-BOUND AND SECRETED FORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 AHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM--N 123
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VIA CARBONYL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                    SMART; SMO0085; PA2c; 1.
PROSITE; PS00118; PA2_HIS; 1.
PROSITE; PS00119; PA2_ASP; 1.
Hydrolase; Lipid degradation; Membrane; Signal; Calcium.
             ARE IDENTICAL AND ARE ENCODED BY A SINCLE GENE.
-1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
P -> L (POLYMORPHISM).
S -> D (IN REF. 8).
W -> E (IN REF. 5).
D -> E (IN REF. 5).
L -> V (IN REF. 5).
A -> S (IN REF. 5).
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les 56;
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41.5%; Pred. No. 3.9e
tive 20; Mismatches
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Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
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                                                                                                                                                      EMBL; D00523; BAA00410.1; -. EMBL; M37127; AAA41223.1; -. EMBL; M25148; AAA41920.1; -. EMBL; X51529; CAA35909.1; -.
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146 AA; 16294 MW;
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PIR; A33506; A33506.
PIR; A35493; A35493.
PIR; JU0131; JU0131.
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PIR; S11388;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                           Morioka Y., Saiga A., Yokota Y., Suzuki N., Ikeda M., Ono T.,
Nakano K., Fujii N., Ishizaki J., Arita H., Hanasaki K.;
"Mouse group X secretory phospholipase A2 induces a potent release of
arachidonic acid from spleen cells and acts as a ligand for the
phospholipase A2 receptor.";
                                                                                                                                                                                                 MEDLINE-20002639; PubMed=10531313; Valentin E., Ghomashchi F., Gelb M.H., Lazdunski M., Lambeau G.; Valentin E., Ghomashchi F., Gelb M.H., Lazdunski M., Lambeau G.; On the diversity of secreted phospholipases A2. Cloning, tissue distribution, and functional expression of two novel mouse group II
                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentla; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GROUP X SECRETORY PHOSPHOLIPASE A2.
                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Group X secretory phospholipase A2 precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase GX) (GX sPLA2.X).
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., SEQUENCE OF 18-30, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMARI, SMOOLO, TESP, 1.
PROSITE; PS00119; PA2_HIS; 1.
Hydrolase; Lipid degradation; Calcium; Signal.
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BY SIMILARITY.
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MCD; MC134752; Pla2910.
Interpro; IPR001211; PhospholipaseA2.
Pfam; PF00068; Phoslip; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
                                                                                                                                                                                                                                                                     enzymes.";
J. Biol. Chem. 274:31195-31202(1999).
                                                                                                                                                                                                                                                                                                                                 MEDLINE=20470496; PubMed=11019817;
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             STANDARD;
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                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=10090;
                           Q9EQK6;
                                                                                                                                                                                                                                                                                                                           STRAIN-BALB/C;
          PA2X_MOUSE
Q9QXX3; Q9EC
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PA2X_MOUSE
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SEQUENCE OF 21-150 FROM N.A.

MEDLINE-9436495; PubMed-8083202;

MEDLINE-94364995; PubMed-8083202;

Chen J., Engle S.J., Seilhamer J.J., Tischfield J.A.;

Chen J., Engle S.J., Seilhamer J.J., Tischfield J.A.;

Chen J., Engle S.J., Seilhamer J., Seilhamer 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97209919; PubMed-9057094; Chn., Lee W., Tischfield J.A.; Chn J., Shoo C., Lazar V., Srivastava C.H., Lee W., Tischfield J.A.; Chail J., Shoo C., Lazar V., Srivastava C.H., Lee W., Tischfield J.A.; Localization of group II to low molecular weight phospholipase A2 mRNA to melotic cells in the mouse."; J. Cell. Biochem. 64:369-375(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acylglycerophosphocholing a fatty acid anion.
-!- COFACTOR: Bands I calcium ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- TISSUE SPECIFICITY: TESTIS-SPECIFIC.
-!- DEVELOPMENTAL STAGE: EXPRESSED MAINLY IN PACHYTENE AND SECONDARY
-!- DEVELOPMENTAL STAGE: EXPRESSED MAINLY IN PACHYTENE AND SECONDARY
-!- DEVELOPMENTAL STAGE: AND ROUND SPERMATIDS AND PREDOMINATES IN STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 YVDHY-----DHTIENNTEIVCSDLNKTECDKQTCMCDKNNVLCLMNQTYREEYRGFLNV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Group IIC secretory phospholipase A2 precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase GIIC) (GIIC spLA2) (PLA2-8) (14
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             22 LLNLKAMVEAVTGRSALLSFVGYGCYCGLGGRGQPKDEVDWCCHAHDCCYQELFDQGCHP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                    VIA CARBONYL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                   29.6%; Score 283.5; DB 1; Length 151; 37.7%; Pred. No. 9.2e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i - CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                    N -> D (IN REF. 2).
05D15E70BC2C9294 CRC64;
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                                                                                                                    VIA CARBONYL OXYGEN
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                            23; Mismatches
                                                                                                                                                                                                BY SIMILARITY
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                                                                                                                                                                                                                                                 17005 MW;
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PLA2G2C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 YCQGPTPNCS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 LCEKDSPKCN 151
                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                 151 AA;
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P48076;
                                                                             DISULFID
                                                                                                                                                                                                     CA_BIND
CONFLICT
                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                      SEQUENCE
          DISULFID
                                 DISULFID
                                                         DISULFID
                                                                                                                                                   CA_BIND
                                                                                                                               CA_BIND
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RESULT 15
PA2A_MOUSE
                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by an one profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/created an email to license@lab-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 PILNAYOFTIVNGTVTCGCTVASSCPCGQKACECDKOSVYCFKENLATYEKAFKQLF--- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 SLLNLKAMVEAVTGRSAILSFVGYGGTGGTGGPKDEVDWCCHAHDCCYQELFDQGCH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 SFWQFQRMYKHYTGRSAFFSYYGYGCLGGGGLGLYVDATDRCCWAHDCCYHKLKEYGCQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .) (POTENTIAL).
EN (BY SIMILARITY).
EN (BY SIMILARITY).
EN (BY SIMILARITY).
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GROUP IIC SECRETORY PHOSPHOLIPASE A2.
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Group X secretory phospholipase A2 precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase GX) (GX SPLA2) (SPLA2-X).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 150;
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-1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M -> W (IN REF. 2).
Y -> W (IN REF. 2).
C2D5EF5E7819972F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIA CARBONYL OXYGEN (VIA CARBO
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Notewith the state of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWART; SW00085; PA2C; 1.
PROSITE; PS00118; PA2_HIS; 1.
PROSITE; PS00119; PA2_ASP; 1.
Hydrolase; Lipid degradation; Calcium; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:106658; Pla2g2c.
InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
ProDom; PD000203; PhospholipaseA2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                   EMBL; U18119; AAC52936.1; -.
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Q9QZT3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
                                                                         enzymes.";
J. Biol. Chem. 274:31195-31202(1999).
-I-FUNCTION: PAZ catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. Has a powerful potency for releasing arachidonic acid from cell membrane phospholipids (By
SEQUENCE FROM N.A.
MEDLINE=20002639; PubMed=10531313;
Valentin E., Ghomashchi F., Gelb M.H., Lazdunski M., Lambeau G.;
"On the diversity of secreted phospholipases A2. Cloning, tissue distribution, and functional expression of two novel mouse group II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 HAHDCCYQELFDQGCHPYVDHY-----DHTIENNTEIVCSDLNKTECDKQTCMCDKNMVL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 YYHDCCYSQAQDAGCSPKLYRYPWKCMDH-----RILCGPA-ENKCQELLCRCDETLAY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 GSVLSTA-----HGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIA CARBONYL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GROUP X SECRETORY PHOSPHOLIPASE A2.
                                                                                                                                                                                    acylglycerophosphocholine + a fatty acid anion.
--- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
--- SUBCELLULAR LOCATION: Secreted.
--- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 282; DB 1; Length 151; Pred. No. 1.3e-18;
                                                                                                                                                                   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y SIMILARITY,
2581E1520A455089 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Lipid degradation; Calcium; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000303; PhospholipaseA2; 1. SMART; SM00085; PA2c; 1. PROSITE; PS00119; PA2_ASP; 1. PROSITE; PS00118; PA2_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 CLMNQTYREEYRGFLNVYCQGPTPNCS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 CLADTEYHLKYLFFPSVLCEKDSPKCN 151
                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF166100; AAF04501.1; -.
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36.7%;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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STRAIN=BALB/C; TISSUE-Small intestine;
MEDLINE=94029955; PubMed=8267767;
Mulherkar R., Rao R.S., Wagle A.S., Patki V., Deo M.G.;
Mulherkar R., Paneth cell specific protein from mouse small intestines: predicted amino acid sequence from RT-PCR amplified cDNA and its expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -; - CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
acylgiycerophosphocholine + a fatty acid anion.
acylgiycerophosphocholine + a fatty acid anion.
-; - COFACTOR: Binds 1 calcium ion per subunit (By similarity).
-; - SUBCELLULAR LOCATION: Membrane-associated.
-; - TISSUE SPECIFICITY: MAINLY IN THE PANETH CELLS ADJACENT TO THE STEM POPULATION IN THE SALL INTESTINES. ALSO EXPRESSED IN RECENERATING LIVER AND HYPERPLASTIC OESOPHAGEAL EPITHELLUM.
-; - SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
             P31452, 060871;
01-J01-1993 (Rel. 26, Created)
01-FBB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
Phosphatidylcholine 2-aylhydrolase) (Group IIA phospholipase A2)
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Siracusa L.D., Buchberg A.M.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mulherkar R., Rao R.S., Wagle A.S., Patki V., Deo M.G.,
Biochem. Biophys. Res. Commun. 197:351-352(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macphee M., Chepenik K.P., Liddell R.A., Nelson K.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 195:1254-1263(1993).
                                                                                                                                                                                                                                                                         (GIIC sPLA2) (Enhancing factor) (EF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in inbred mouse strains.";
J. Biol. Chem. 270:22378-22385(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94071967; PubMed=8250944;
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10090;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                        PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 HAHDCCYQELFDQGCHPYVDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM-- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 ILAGSVLSTA----HGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCC 64
                                                                                                                                                                                                                                                                                                                                                                                                    VIA CARBONYL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
BY SIMILARITY.
D -> V (IN REF. 2).
T -> K (IN REF. 2 AND 3).
WW; E3182F68241CC5D2 CRC64;
                                                                                                                                                                                                    SMART; SMO0085; PA2C; 1. PROSITE; PS00118; PA2_ASP; 1. PROSITE; PS00119; PA2_ASP; 1. Hydrolase; Lipid degradation; Calcium; Growth regulation; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.4%; Score 281; DB 1; Length 146; 37.1%; Pred. No. 1.5e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: February 10, 2003, 10:35:49
                                                                                                                                    HSSP; P14555; 1POD.
MGD; MGI:104642; P1a292a.
InterPro; IPR001211; PhospholipaseA2.
                                                                                                                                                                                           PD000303; PhospholipaseA2; 1.
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50 VI.
52 VI.
69 BY
19 D
86 T
                                                                                                                                                                  Pfam; PF00068; phoslip; 1. PRINTS; PR00389; PHPHLIPASEA2.
                                                                                EMBL, X74266; CAA52325.1; -. EMBL, U32358; AAC52252.1; -. EMBL; U28244; AAB06315.1; -.
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146
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(without alignments)
1116.642 Million cell updates/sec
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                                                                                                             February 10, 2003, 10:35:28; Search time 31 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                671580 seqs, 206047115 residues
                                                                     OM protein - protein search, using sw model
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Sp_archea:*
Sp_bacteria:*
sp_fung1:*
sp_human:*
sp_lnvertebrate:*
sp_mammal:* sp_unclassified:* sp_vertebrate:* sp_rvirus:*
sp_bacteriap:* sp_organelle:* sp_archeap:* sp_rodent:* sp_plant:* sp_virus:* sp_phage: * sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

094x68 mesocricetu 091y34 rattus norv 042188 agkistrodon 090w39 trimeresuru 090z29 echis color 090395 crotalus sc 080wz6 crotalus at 042192 agkistrodon 042187 agkistrodon 091968 trimeresuru trimeresuru OBuvu8 bothriechis O42187 agkistrodon crotalus at Q9h415 homo sapien Description Q8uvz7 SUMMARIES 091Y34 042188 Q90Y77 **Q8UVU8** 091968 Q90W39 090395 042192 **08UV27 080VU7** Query Match Length DB 30.8 30.8 30.3 30.3 30.3 229.7 229.0 227.5 27.5 Score 290 287.5 284.5 280.5 277.5 269.2 267.5 263.5 263.5 263.5 263.5 294.5 290.5 Result

			092151 trimeresuru P79836 trimeresuru P79836 trimeresuru O9pvf1 agkistrodon O9pvf0 agkistrodon O9pvf0 agkistrodon O9pvf0 alcentrarch O9df52 bungarus ca O9uwal lapemis har O90wa8 bungarus fa O90wa7 bungarus fa
52 221 67	8 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	8 8 9 1 0 0 0 5 7 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	781722224
092152 09PVF3 091521 042190 091967	092118 091AT9 042189 09PWR6 08UVZ5 057385	Q9PVF4 Q9PVF2 Q91506 Q910A0 Q910A1 Q9PVE9	0976151 0976151 097617 098760 098760 090852 090831
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137 122 124 137	138 138 138 138	133 133 138 138 139	137 126 126 145 145 145 145
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17 18 20 21 22	23 25 27 28 28	20 33 33 34 36 37	37 38 38 44 44 55

ALIGNMENTS

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                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DJ340N1.1 (Novel phosphollpase similar to mouse phospholipase A2 group DJ340N1.1.
                                                                                                                                                                                                                                                                                                                                                                                                                          100 DLNKTECDKQTCMCDKNMVLCLMNQTYREEYRGFLNVYCQGPTPNCSIYEPPPEEVTCSH 159
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                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                    42.0%; Score 402; DB 4; Length 69; 100.0%; Pred. No. 5.3e-37; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                 Bird C.; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL; 298257; CACL12707.1; -. InterPro; IFF001211; PhospholipaseA2. Pfam; PF00068; phoslip; 1. ProDom; PD000303; PhospholipaseA2; 1.
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                                  69 AA.
                                  PRT;
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Matches 69; Conservative
                               PRELIMINARY;
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Q9H4I5;
RESULT 1
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RESULT 2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDILNE=21478853; PubMed=11594738;
Tsai I.H., Chen Y.H., Wang Y.M., Tu M.C., Tu A.T.;
Trai I.H., Chen Y.H., Wang Y.M., Tu M.C., Tu A.T.;
"purification, Sequencing, and Phylogenetic Analyses of Novel Lys-49 phospholipases A(2) from the Venoms of Rattlesnakes and other Pit
                                                                                                                                                                                                                                                                                                                                                                                                  h
Similarity 40.1%; Pred. No. 1.7e-27;
59; Conservative 28; Mismatches 49; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chījiwa T., Yamaguchi Y., Ogawa T., Deshimaru M., Nobuhisa I.,
Nakashima K., Oda-Ueda N., Shimohigashi Y., Fukumaki Y., Hattori S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lys-49 phospholipase A2-like protein.

Lys-49 phospholipase A2-like protein.

Bothriechis schlegelii (Eyelash palm pitriper).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Bothriechis.
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                 Regional evolution of Trimeresurus flavoviridis venom-gland
                                                                                                                                                                                                                                                                     Submitter (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL, ABG7173: BAB68546.1; ... Interpro; IPR001211; PhospholipaseA2.
                                                                                                                                                                                                                                                                                                                                    Probom; PD000303; PhospholipaseA2; 1.
PROSTTE; PS00119; PA2_ASP; UNKNOWN_1.
PROSTTE; PS00118; PA2_HIS; UNKNOWN_1.
SEQUENCE 138 AA; 15729 MW; C96BIE878CCA1196 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arch. Biochem, Biophys. 394:236-244(2001).
EMBL, AF374236; AAL39065.1;
InterPro; IPR001211; PhosspholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
Probom; P0000303; PhospholipaseA2; 1.
                     138 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                     PRT;
                                                                                                                    Trimeresurus flavoviridis (Habu).
                                                                                        Phosphlipase A2 isoenzyme PL-Y.
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                        PRELIMINARY;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=44725;
                                                                                                                                                                                                                                                                                                                                                                                                                                       59;
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                        090Y77
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
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           Q90Y77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 SLLNLKAMVEAVTGRSAILSFVGYGGYGGLGGRGQPKDEVDWCCHAHDCCYQELFDQGCH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Gaps
                                                                                                                                                                                                                                            61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                             1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                   1 MRILWIVAVL----LVGVEGSMYELGKMILLETGKNAATSYIAYGCNCGVGRRGQPLDAT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
NCBI_TaxID-8714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys
                                                              30.8%; Score 294.5; DB 13; Length 122; llarity 40.9%; Pred. No. 8.5e-25; Conservative 23; Mismatches 45; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pan H., Wu X.F., Ouyang L.L., Liu X.L., Yang G.Z.; "CDNA of phospholipase A2 from Agkistrodon halys Pallas."; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF015242; ABB71844.1; "HSSP; P51922; IVAP. InterPro; IPR001211; PhospholipaseA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 122 AA; 13892 MW; 4980C6AA5E648EAE CRC64;
PROSITE; PSO0119; PA2_ASP; UNKNOWN_1.
PROSITE; PSO0118; PA2_HIS; UNKNOWN_1.
SEQUENCE 137 AA; 15285 MW; 0D588DE1AC84D00D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 122 AA.
                                                                                                     40.6%; Pred. w. +ive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
SMART; SM00085; PA2c; 1.
                                                                                                                                                                                                                                                                                                                                     121 LMN--QTYREEYRGFLNVYCQGP 141
                                                                                                                                                                                                                                                                                                                                                                           112 LGKNVNTYNKNYKITMKMFCKKP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00119; PA2_ASP; 1. PROSITE; PS00118; PA2_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phospholipase A2 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                   58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 52; Conserv
                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mizenina O., Musatkina E., Yanushevich Y., Rodina A., Krasilnikov M., De Gunzburg J., Camonis J., Tavitian A., Tatosyan A.;
"A novel group IIA phospholipase A2 interacts with v-Src oncoprotein from RSV-transformed hamster cells.";
J. Blol. Chem. 27606:34006-34012(2001).
HSSP, p14555; 1P0D.
HIGHERO: IPR001211; PhospholipaseA2.
Pfam: PF00068; Phosilp: 1.
PRINTS: PR00389; PHPHLIPASEA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Phospholippse a precursor (EC 3.1.1.4).
Trimeresurus mucrosquamatus (Taiwan habu).
Eukaryota: Metazoa; Chordets, Craniata: Vertebrata; Euteleostomi; Lepidosauria; Squamata: Scleroqlossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mesocricetus auratus (Golden hamster).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Src-associated phospholipase A2 precursor (EC 3.1.1.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN 17 138 PHOSPHOLIPASE A2.
SEQUENCE 138 AA; 15739 MW; BFCBD597BF9A36C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00068; phositp; 1.
PRINTS; PR00189; PHPHLIPASEA2.
ProDom; PD00013; PhospholipaseA2; 1.
SMART; SM00085; PA2c; 1.
PROSITE; PS00119; PA2_ASP; 1.
PROSITE; PS00119; PA2_ASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001211; PhospholipaseA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 FLNNLGTYNEEYNNYRKSRCIEESPKC 138
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                                                                                                                                                                                                                                                                                                                                                         EMBL; X77646; CAB88411.1; -. HSSP; P51972; IVAP.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-SNAKE VENOM GLAND;
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                                                                                                                                                                                                          NCBI_TaxID=103944;
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Q9QX68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEWBLrel. 19, Created)
01-DEC-2001 (TrEWBLrel. 19, Last sequence update)
01-DEC-2001 (TrEWBLrel. 11, Last sequence update)
01-JUN-2002 (TrEWBLrel. 12, Last annotation update)
Platelet phospholipase A2 precursor (Fragment).
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID-10116;
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 AHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM--N 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-WISTAR; TISSUE-BLOOD; Liu T.T., Liang N.S., Meng Z.Q., Xie Y.A., Kuang Z.P., Li Y.; "Cloning and sequence determination of rat platelet phospholipase A2
                                                                                                                                                                                                                                                  20 GSLINLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCCHAHDCCYQELFDQGC 79
                                                                                                                                                                                                                                                                            7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 VAILA-GSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCCH 65
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                                                                                        SRC-ASSOCIATED PHOSPHOLIPASE A2. F5E0A76CE441772C CRC64;
                                                                                                                                                            Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.0%; Score 287.5; DB 11; Length: 41.5%; Pred. No. 6.2e-24; tive 19; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from whole blood.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AF365363, AAK52061.1;
InterPro; IRR001211; PhospholipaseA2.
ProDom: PF00068; phoslip; 1.
PROSITE; PS00119; PA2_ASP; UNKNOWN_1.
PROSITE; PS00119; PA2_ASP; UNKNOWN_1.
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PLATELET PHOSPHOLIPASE A2.
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                                                                                                                                                         30.3%; Score 290; DB 11;
44.2%; Pred. No. 3.5e-24;
tive 17; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 AA.
                                                                     POTENTIAL
PROSITE; PS00119; PA2_ASP; UNKNOWN_1. PROSITE; PS00118; PA2_HIS; UNKNOWN_1.
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                                                                                                             SEQUENCE 154 AA; 17217 MW;
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Matches 59; Conservative
                                                                                                                                                                                                      57; Conservative
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>146
                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 138 CQGPTPNCS 146
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                                            Hydrolase; Signal.
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SEQUENCE
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Q91Y34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 PKWDDYTYSWKNGT-IVCG--GDDPCKKEVCECDKAAAICFRDNLKTYKKRYMTYPNILC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 SLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEVDWCCHAHDCCYQELFDQGCH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Protobothrops.
NCBL_TaxID=103944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pāllas).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
NCBI_TaxID=8714;
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF408409. AAK97534.1;
InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00008; PhoSlip. 1.
Probom: PD0000303; PhospholipaseA2;
Probom: PS000199; PA2_ASP; UNKNOWN_1.
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SEQUENCE 122 AA; 13876 MW; 877B271DE312EF6A CRC64;
                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Acidic phospholipase A2 (EC 3.1.1.4).
                                                                                                                       122 AA.
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                                                                                                                       PRT;
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Matches 49; Conservative
                                                                                                                       PRELIMINARY;
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RESULT 8
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                                                                                                                                                                                                       1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Echis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kordis D., Gubensek F.;

"Evolutionary relationships of Viperidae phospholipase A2 genes "Evolutionary relationships of Viperidae phospholipase A2 genes unferred (From intron deces."; Decess.")

EMBL, AF253050; AAK49823.1; -.

EMBL, AF253050; AAK49823.1; -.

FinterPro; IPR001211; PhospholipaseA2.

Probom; PF00068; phoslip; 1.

Probom; PF00068; phoslip; 1.

PROSITE; PS001119; PA2_ABS; UNKNOWN_1.

SEQUENCE 138 AA; 15770 WW; 1A5D9F17FDAA9D56 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 21, Last annotation update)
Phospholipase A2 precursor (EC 3.1.1.4) (Phosphatidylcholine 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.0%; Score 277.5; DB 13; Length 138; 36.7%; Pred. No. 7.5e-23; ive 25; Mismatches 57; Indels 11;
                                                                                                  DB 13; Length 138;
                                               15668 MW; AA8542A33DF52AB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                             29.3%; Score 280.5; DB 13; 37.4%; Pred. No. 3.5e-23; tive 29; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 AA.
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PROSITE; PS00118; PA2_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                               121 LMN--QTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 LGHNLRTYKKRYMFYPDFLCTDPSEKC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
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Matches 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                  138 AA;
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                                                  SEQUENCE
                                                                                                     Query Match
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Q92147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphisms of Trimeresurus flavoviridis venom gland phospholipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRCCFVHDCCYGKV--TGCDPKDDFYIYSSENG-DIVCGD--DDLCKKEVCECDKAAAIC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Accelerated evolution in the protein-coding regions is universal in crotalines snake venom gland phospholipase A2 isozyme genes."; Proc. Natl. Acad. Sci. U.S.A. 92:5605-5609(1995).
-:- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)0 = 1- ACYLGLYCEROPHOSPHOCHOLINE + A FATTY ACID ANION.
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acylhydrolase) (Lecithinase A) (PHOSPHATIDASE) (PHOSPHATIDOLIPASE)
Trimeresurus flavoviridis (Habu).
                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93317604; PubMed-8327468;
Nakashima K., Ogawa T., Oda N., Hattori M., Sakaki Y., Kihara H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Accelerated evolution of Trimeresurus flavoviridis venom gland phospholipase A2 isozymes.";
Proc. Natl. Acad. Sci. U.S.A. 90:5964-5968(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95296360; Pubmed-7777556;
Nakashima K., Nobuhisa I., Deshimaru M., Nakai M., Ogawa T.,
Shimohigashi Y., Fukumaki Y., Hattori M., Sakaki Y., Hattori S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 138;
                                                                                                                                                                                                                                                                                                                 Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHOLIPASE A2. AAD7DC04A6EDA975 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.1%; Score 269; DB 13; 37.7%; Pred. No. 6.5e-22; tive 21; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A2 isozyme genes.";
Biosci. Biotechnol. Biochem. 58:1510-1511(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94369106; PubMed=7765285;
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PROSITE; PSOOLIUS; PA2_ASP; 1.
PROSITE; PSOOLIUS; PA2_HIS; 1.
Hydrolase; Polymorphism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN 17 138 P
SEQUENCE 138 AA; 15708 MW;
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EMBL; D10723; BAA01568-1; -.
EMBL; D10723; BAA01566-1; -.
HSSP; P14418; 1BK9.
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Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                        NCBI_TaxID=88087;
                                                                                                                                                                                                                                                     TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PISSUE-LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LISSUE-LIVER
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SEQUENCE FROM N.A. Trans, Wang Y.-M., Tu A.T.; Taal I.-H., Chen Y.-H., Wang Y.-M., Tu A.T.; Cloning, characterization and phylogeny of two novel Lys-49 phospholipase A2 from Crotalus atrox and Delnagkistrodon acutus venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-LIVER;
MEDITNE-94156205; PubMed-8112610;
MEDITNE-94156205; PubMed-8112610;
John T.R., Smith L.A., Kalser I.I.;
"Genomic sequences encoding the acidic and basic subunits of Mojave toxin: unusually high sequence identity of non-coding regions.";
Gene 139:229-234(1994).
HSSP; P00624; IPP2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Preproacidic subunit of mojave toxin precursor.
Crotalus scutulatus scutulatus (Mojave rattlesnake)
Bukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroldea;
Viperidae; Crotalinae; Crotalus.
NGBI_TaxID=8730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROACIDIC SUBUNIT OF MOJAVE TOXIN.
8164C7C8D27D6EBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13; Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glands.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Acidic phospholipase A2 precursor.
Crotalus atrox (Western diamondback rattlesnake).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.0%; Score 267.5; DB 1
38.8%; Pred. No. 9.6e-22;
tive 18; Mismatches 61
                                                               138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
SWART; SW00085; PA2C; 1.
PROSITE; PS00119; PA2_ASP; 1.
PROSITE; PS00118; PA2_ASF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 LMN--QTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 FRDSMNTYDYKYLRFSPENCOGESOPC 138
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                                                               PRT;
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138 PR
15211 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 38.8%
Matches 57; Conservative
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                                                               PRELIMINARY;
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CHAIN 17 ]
SEQUENCE 138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8738;
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                                                               090395
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RESULT 12
                          090395
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141 PTPNCSIYEPP 151 | || || 1 111 PAKNCQEESEP 121

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                                                                                                                                                                                                                                                                                                                                                                                 81 PYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLMNQTYREEYRGFLNVYCQG 140
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                                                                                                                                                                                                                                                                                             1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                                                                                                                                             1 MRTLWIVAVL----LLGVEGSLVQFETLIMKIAGRSGLLWYSAYGCYCGWGGHGLPQDAT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Phospholipase A2 (Fragment).
Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys
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Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
NCBI_TaxID=8714;
                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                           27.5%; Score 263.5; DB 13; Length 138; 36.8%; Pred. No. 2.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.5%: Score 263; DB 13; Length 122; 39.7%: Pred. No. 2.6e-21; Live 18; Mismatches 51; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan H., Wu X.F., Ouyang L.L., Liu X.L., Yang G.Z.; "CDMA of phospholipase A2 from Agkistrodon halys Pallas."; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF015247; AAB71849.1; -. HSSP; P14418; 1BK9.
                                                                                                                                                          POTENTIAL.
ACIDIC PHOSPHOLIPASE A2.
78A0034CA963A4E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER 1 1 1
SEQUENCE 122 AA; 13666 MW; C7D21D90CBE1F314 CRC64;
                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                            20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               121 LMNQTYREEYRGFLNVYCQGPTPNCSIYEPPP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 ----FRDNIPSYDNKYWLFPPKNCR-EEPEP 137
EMBL, AF269131; AAL36974.1; -.
InterPro: IPR001211; PhospholipaseA2.
Pfam; PF00068; Phoslip; 1.
PRIWTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
SMART; SW00085; PA2C, 1.
PROSITE; PS00119; PA2_ASP; UNKNOWN.1.
PROSITE; PS00118; PA2_HIS; UNKNOWN.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro: IPR001211; PhospholipaseA2.
Prêma, PP00068; phostb; 1.
PRINTS; PR00189; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
SMART; SW00085; PA2.C; 1.
PROSITE; PS00119; PA2.ASP; 1.
PROSITE; PS00118; PA2.AIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                          SIGNAL 1 16 PV
CHAIN 17 138 AV
SEQUENCE 138 AA; 15346 MW;
                                                                                                                                                                                                                                          Local Similarity 36.8% nes 56; Conservative
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Matches 52; Conservative
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                                                                                                                                                                                                                            Query Match
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SIGNAL
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[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. TA A.T.; Taal I.-H., Chen Y.-H., Wang Y.-M., Tu A.T.; Taal I.-H., Chen Y-H., Wang Young two novel Lys-49 "Cloning, characterization and phylogeny of two novel Lys-49 phospholipase A2 from Crotalus atrox and Deinagkistrodon acutus venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DWCCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKFFTVAILAGSVLSTAHGSLLNLKAMVEAVTGRSAILSFVGYGCYCGLGGRGQPKDEV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Verrebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.4%; Score 262.5; DB 13; Length 137; 39.2%; Pred, No. 3.4e-21; ative 27; Mismatches 49; Indels 11;
                                                                                                                                                                                                                                                                                                           glands.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UJN-2002 (TrEMBLrel. 21, Last annotation update)
Lys-49 phospholipase A2 precursor.
Crotalus atrox (Western diamondback rattlesnake).
                                   137 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00085; PA2c; 1.
PROSITE; PS00119; PA2_ASP; UNKNOWN_1.
PROSITE; PS00118; PA2_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                           EMBL; AF269130; AAL36973.1; -
InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
Probom; PD000303; PhospholipaseA2; 1.
                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LMN--QTYREEYRGFLNVYCQGP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
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les 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal.
SIGNAL
                                 Q8UVZ7
                                                     Q8UVZ7
RESULT 15
Q8UVZ7
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